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Search time 18.33 Seconds (without alignments) 424.776 Million cell updates/sec
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                                                                      4, 2002, 14:43:11;
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Issued\_Patents\_AA:\*

: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*

: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*

: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*

!: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*

: /cgn2\_6/ptodata/2/iaa/FCTUS\_COMB.pep:\*

: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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m	7	2.0	П	4	-08-905-223-4	39,
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9	7	2.0	8	4	-08-785-42	2, 4
7	7	2.0	4	~	-08-676-279-	ce 59,
ω	9	1.7	11	4	-09-196-293-	7, 1
δ	9	1.7	11	4	S-08-209-60	7, 1
10	9	1.7	13	5	S94-10257A-	52,
11	φ	1.7	15	7	-08-378-761A-	48,
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19	9	1.7	18	7	-08-932-682-13	134
20	9	1.7	20	ហ	T-US94-10257A-8	0,
21	9	1.7	21	↤	-08-786-748A-12	m
22	9	1.7	21		-786-748A-12	9
23	9	1.7	21	٦	-786-748A-	Sequence 127, App
24	9		21	Ţ	-786-748A-13	35
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26	9		21	7	-682-12	ᠬ
27	9		21	7	-932-682-12	9

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Gaps

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Length 346;

DB 2;

Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 346; Conservative 0; Mismatches

Sequence 127, App Sequence 135, App Sequence 137, App Sequence 17, Appl Sequence 26, Appl Sequence 5, Appl Sequence 45, Appl Sequence 25, Appl		
28 6 1.7 21 2 US-08-932-682-127 29 6 1.7 21 2 US-08-932-682-135 30 6 1.7 21 2 US-08-932-682-137 31 6 1.7 21 2 US-08-988-856B-17 32 6 1.7 67 4 US-08-988-856B-17 33 6 1.7 104 3 US-08-461-990B-26 33 6 1.7 116 2 US-08-960-022-16 35 6 1.7 127 1 US-08-982-882-45 36 6 1.7 127 2 US-08-483-889-45 40 6 1.7 127 2 US-08-483-89-45 41 6 1.7 127 2 US-08-483-932-45 42 6 1.7 127 2 US-08-473-503-45 43 6 1.7 127 2 US-08-473-680-45 44 6 1.7 127 3 US-08-475-680-45 45 6 1.7 127 3 US-08-475-680-45 46 1.7 127 3 US-08-475-680-45 47 105 105-07-929-580B-2	RESULT 1  UG-08-613-220B-4  Sequence 4, Application US/0861320B  Patent No. 5958751  GENERAL INFORMATION: APPLICANT: Murphy, Dennis APPLICANT: Reid, John TITLE OF INVENTION: ALPHA-GALACTOSIDASE COMPLESSEE: Fish & Richardson, P.C. STREET: 4225 Executive Square, Suite 1400 CITY: La Johla STRATE: CA COUNTRY: US ZIP: 9203 ZIP: 9203 ZIP: 1000 SYSTEM: Windows Version 2.0 COMPUTER: IBM Compatible OPERATING SYSTEM: Windows Version 2.0 CURRENT APPLICANTION DATA: APPLICATION NUMBER: US/08/613,220B FILING DATE: OB-MAR-1996 CLASSIFICATION NUMBER: FILING DATE: APPLICATION NUMBER: REGISTRATION NUMBER: FILING DATE: APPLICATION NUMBER: APPLICATION NUMBE	TYPE: amino TOPOLOGY: li MOLECULE TYPE: FRAGMENT TYPE: IS-08-613-220B-4

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sanders, Jan W.

APPLICANT: Ledeboer, Adrianus M.

APPLICANT: Ledeboer, Adrianus M.

APPLICANT: Ledeboer, Adrianus M.

APPLICANT: Ledeboer, Adrianus M.

APPLICANT: Venema, Gerard

APPLICANT: Venema, Gerard

APPLICANT: Venema, Gerard

APPLICANT: Venema, Gerard

TITLE OF INVENTION: Bacterium, and its Use in a Lacctic Acid Bac;

TITLE OF INVENTION: Production of Desired Protein

FILE REFERENCE: Sanders-60113/025227

CURRENT APPLICATION NUMBER: US/09/068,195B

CURRENT FILING DATE: 1998-07-29

EARLIER FILING DATE: 1997-08-20

EARLIER APPLICATION NUMBER: EP 97200744/7

EARLIER APPLICATION NUMBER: EP 96202444/4

EARLIER PILING DATE: 1996-09-05

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0
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                                                                  Length 466;
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Mismatches
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Aymeric
Bruno
5' ESTs FOR SEG
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100.0%; Pi
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Duelert,
Lacroix,
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8; Conser
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Sequence 25, A
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US-09-068-195-25
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APPLICANT:
APPLICANT:
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LENGTH: 466
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NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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; OTHER INFORMATION: Seq ILPLLFGCLGVFG/LF
US-08-905-223-439
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                                                                                                                                                                                                                       US/08/905,223
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APPLICANT: Bandman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 439;
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.0%; Sc.
100.0%; Pr
                                                                                                COUNTRI. CL. ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                         CLASSIFICATION: 55.
CLASSIFICATION: 55.
                                                                                                                                                                           Win95
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                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskett
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Best Local Similarity
Matches 7; Conser
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ORIGINAL SOURCE:
ORGANISM: HOMG
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27 TAILPLL 33
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Gaps

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RESULT 6
US-08-785-427-2
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red. No. 52;
Mismatches
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSEE: SmithKline Beecham Corporation
7: 709 Swedeland Road
King of Prussia
                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,298
FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                   NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0453 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFRAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vers
17-JAN-1997
N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08913578
Patent No. 6218159
GENERAL INFORMATION:
APPLICANT: Hodgson, John
APPLICANT: Lawlor, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                      2.0%; SU
100.0%; Pi
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19-JAN-1996
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Elizabeth
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Diskette
IBM Compatible
SYSTEM: DOS
IBM Compatible SYSTEM: DOS
                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                        amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acid
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                   single
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Lawlor, F
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TOPOLOGY: lin
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STREET: 70
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COMPUTER:
OPERATING
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US-08-913-578-2
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STATE:
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                                                                                                                                                                                                                                                                                                                                         CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
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                                                                                                                                                                                                                                             sequence 2, Application US/08785427
patent No. 6238900
general Information:
    APPLICANT: Hodgson, John
    TITLE OF INVENTION:
    TITLE OF INVENTION:
    APPLICANT: Lawlor, Elizabeth
    TITLE OF INVENTION: No. 6238900el tRNA synthetase
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Smithkline Beecham Corporation
    STREET: 709 Swedeland Road
    CITY: King of Prussia
    STATE: PA
    COUNTRY: USA
    ZIP: 1
                                                                                                                                                                                    0;
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                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,427
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                                                                                                                                                    Score 7; DB 4
Pred. No. 81;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 7; DB 4; Pred. No. 81; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TION DATA:
JMBER: US/08/785,427
17-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 9601069.9
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31352
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38,891
R: P31352
                                                                                                                                         2.0%; Sc.
100.0%; P
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100.0%;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                               484 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                             single
                                                                                         peptide
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APPLICATION NUMBER:
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                                                                                                                                 Query Match
Best Local Similarity
                                                         ; STRANDEDNESS: Sin
; TOPOLOGY: linear
; MOLECULE TYPE: pept
US-08-913-578-2
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les 7; Conser
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342 LPHLIKA 348
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342 LPHLIKA 348
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MOLECULE TYPE:
S-08-785-427-2
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HYPOTHETICAL:
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STREET: 99
CITY: NEW
STATE: NY
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-08-209-603E-7
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US-09-196-293-7
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                                                                                                                                           CURRENT APPLICATION NUMBER: US/08/676 270

FILING DATE:

Luppy disk

Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

FILING DATE:
PRIOR APPLICATION NUMBER: US/08/676 270
                                                                                                                         MACROPHAGE NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09196293

Fatent No. 6183755

GENERAL INFORMATION:

APPLICANT: Fuchs, Renate
APPLICANT: Motz, Manfred
APPLICANT: Milske, Bettina
APPLICANT: Wilske, Bettina
TITLE OF INVENTION: Active proteins from Borrelia
FILER REFERENCE: 738.001082

CURRENT FILING DATE: 1998-11-19

EARLIER APPLICATION NUMBER: WO PCT/EP90/02282

EARLIER APPLICATION NUMBER: WO PCT/EP90/02282

EARLIER APPLICATION NUMBER: DE P39 42 728.5
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/GB95/00095
APPLICATION NUMBER: GB 9400929.7
FILING DATE: 19-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER FILING DATE: 1989-12-22
EARLIER APPLICATION NUMBER: DE P40 18
EARLIER FILING DATE: 1990-06-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                              GB 9422021.7
                                               Sequence 59, Application US/08676279 Patent No. 5869247 GENERAL INFORMATION:
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Q ID NO: 59:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.0%;
                                                                                                                                       NUMBER OF SEQUENCES: 63
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549 amino acids
amino acid
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19-JAN-PRIOR APPLICATION DATA:
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FILING DATE: 31-OC'
INFORMATION FOR SEQ ID
                                                                                                                         TITLE OF INVENTION:
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                SULT 7
-08-676-279-59
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US-08-676-279-59
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                                                                                                     APPLICANT:
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                Length 11;
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APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-MURSIC, VERA
APPLICANT: MOTZ, MANFRED
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE PROTEINS
TITLE OF INVENTION: FROM BORRELIA BURGDORFERI
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                   ;
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1: 99 PARK AVENUE
NEW YORK
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                DB 4;
                                 23;
             Score 6; DB 4
Pred. No. 23;
0; Mismatches
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MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: AT&T - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9217-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,603E
FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/EP90/02282
FILING DATE: 21-DEC-1990
APPLICATION NUMBER: US 07/862,535
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      Sequence 7, Application US/08209603E
Fatent No. 6248538
GENERAL INFORMATION:
APPLICANT: FUCHS, RENATE
APPLICANT: WILSKE, BETTINA
APPLICANT: PREAC-MURSIC, VERA
APPLICANT: SOUTSCHECK, ERWIN
TITLE OF INVENTION: FROM BORRELIA
1.7%; Scu
100.0%; Pi
0;
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; PUBLICATION INFORMATION:
US-08-209-603E-7
                                                     Conservative
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GY: LINEAR
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POSITION IN GENOME:
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               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: N/A
FRAGMENT TYPE: N,
ORIGINAL SOURCE:
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LIBRARY: DSM 5
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MOLECULE TYPE:
DESCRIPTION: 1
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LENGTH:
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Best Local 3
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GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF
RELATED TO AUTOIMMUNE DISEASE
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                                               Indels
                  Length 11;
                                                                                                                                                                                                                                                                                                                                       3: IMMULOGIC PHARMACEUTICAL CORPORATION 610 LINCOLN STREET
                                                                                                                                                                                                      APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION
APPLICANT: BRIGITTE DEVAUX
APPLICANT: JONATHAN B. ROTHBARD
APPLICANT: DAWN SMILEK
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCY
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE POI
TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEAS
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                DB 4;
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Pred. No. 27;
0; Mismatches
               Score 6; DB 4
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/10257A FILING DATE: 1 SEPTEMBER 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,976
3R: 071.1 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: US 08/116,824
03-SEP-1993
                                                                                                                                                            PCT-US94-10257A-52; Sequence 52, Application PC/TUS9410257A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-378-761A-48
; Sequence 48, Application US/08378761A
; Patent No. 5635384
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
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100.0%; P<sub>3</sub>
      1.7%; SC.
100.0%; P.
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DC
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
internal
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                                             Conservative
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 03-SE
CLASSIFICATION:
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Best Local Similarity
5; Conserva
Query Match
Best Local Similarity
Local 6; Conserva
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STATE: Massac
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; MOLECULE TYPE:
; FRAGMENT TYPE:
PCT-US94-10257A-52
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                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                        250 SVEGLL
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                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                  RESULT
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WALSH, TENCETY D
HEY, TIMOTHY D
MORGAN, ALICE ER
VENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
VENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
VENTION: USING
FEQUENCES: 81
                                                                      Q
                                                    RIBOSOME-INACTIVATING PROTEINS, INACTIVE PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 15;
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.7%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 48 SEQUENCE CHARACTERISTICS:
 WALSH, TERENCE A
HEY, TIMOTHY D
MORGAN, ALICE ER
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                      USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC compe
OPERATING SYSTEM: PC-I
SOFTWARE: Patentin Rel
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APPLICANT: WALSH, TERRAPPLICANT: HEY, TIMOTHAPPLICANT: MORGAN, ALTITLE OF INVENTION: PITTLE OF INVENTION: USENUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: WALSH, 7
APPLICANT: HEY, TIN
APPLICANT: MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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6; Conser
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CLASSIFICATION:
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US-08-378-761A-48
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVE FORMS OF MAIZE RIBOSOME INACTIVE PRECURSOR

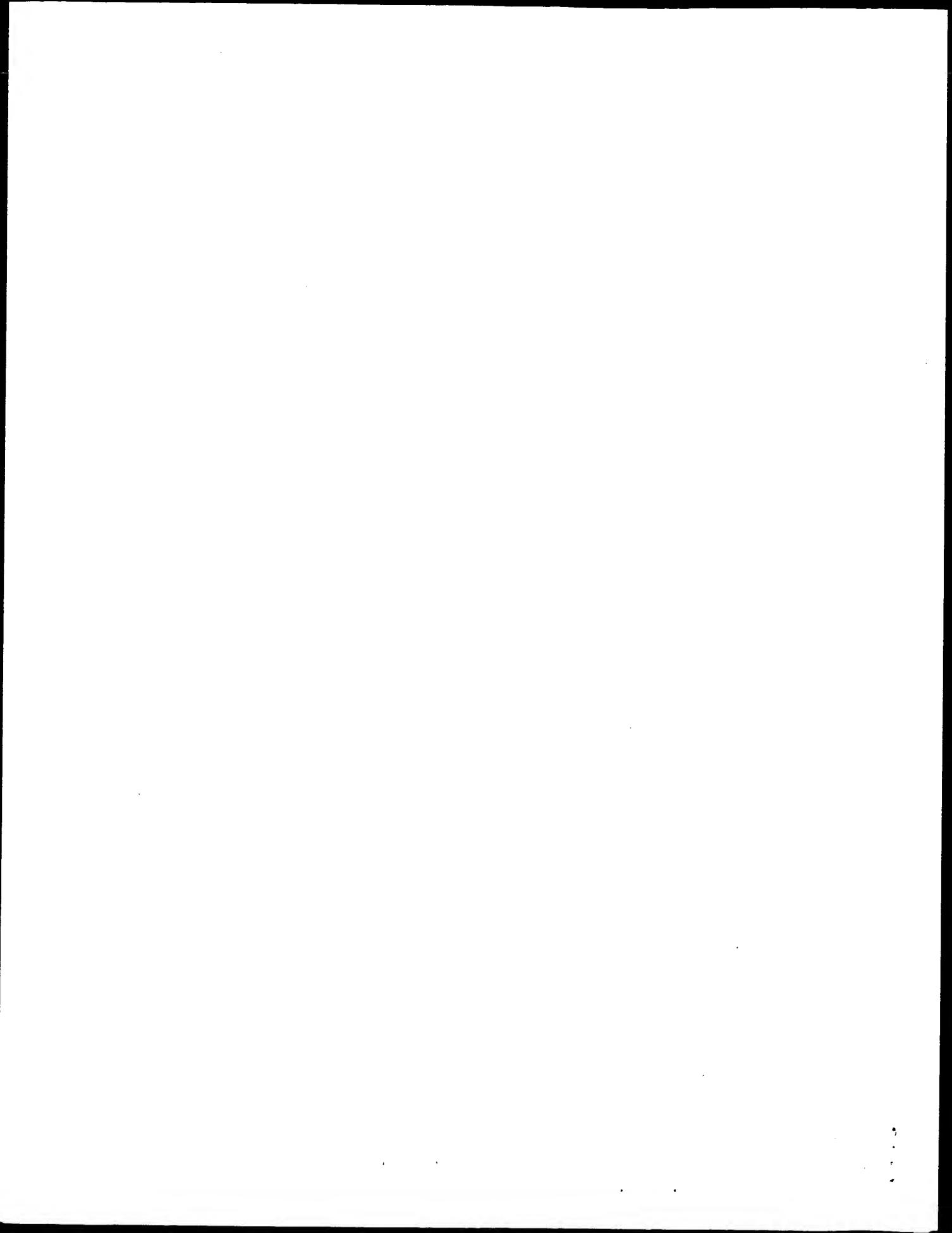
NUMBER OF SEQUENCES: 49

CURRENT APPLICATION DATA:

APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                       ; APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                         0;
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Pred. No. 31;
; Mismatches
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Pred. No. 31;
); Mismatches
                                                    Score 6;
           US/08/485,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 128, Application US/08786748A Patent No. 5714577 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.78; Sc. 100.08; P<sub>3</sub>
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0
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                                                                                                                                                                          15 amino acids
DATA
                                                                                                                                                                                                                                                                                       Conservative
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                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                 single
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RRENT APPLICATION D
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS: sin
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Best Local Similarity
                                                                                                                                                                                                           linear
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nes 6; Conser
                      FILING DATE:
CLASSIFICATION:
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US-08-485-286-48
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10 RFRYIS 15
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5248606-29
; Patent No. 5248606
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248606-29
                                                                                                                                                                                                                                                                                                              163 RFRYIS
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                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                          LENGTH:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5714577
GENERAL INFORMATION:
APPLICANT: Ronald, Montelaro C.
APPLICANT: Tencza, Sarah B.
APPLICANT: Mietzner, Timothy A.
TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
                                                                        SOFTWARE: FASTSEX ...
SOFTWARE: FASTSEX ...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,748A
FILING DATE: 24-JAN-1997
FILING DATE: 514
                                                                                                                                                                                          APPLICATION NUMBER: 60/010,634
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Rochelle K. Seide
REGISTRATION NUMBER: 32,300
REFERENCE/DOCKET NUMBER: AP30421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 132, Application US/08786748A Patent No. 5714577
                                                                                                                                                                                                                                                                                         AP30421
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5714577e
               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPAtible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                       DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                     OPERATING SYSTEM:
10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: New York
COUNTRY: USA
ZIP: 10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE MEDIUM TYPE: Di
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: 11;
; MOLECULE TYPE:
US-08-786-748A-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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3 GLLEVI
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### TELEPHONE: 212-408-2500
| TELEPHONE: 212-765-2519
| INFORMATION FOR SEQ ID NO: 132:
| SEQUENCE CHARACTERISTICS:
| SEQUENCE CHARACTERISTICS:
| TYPE: amino acid |
| MOLECULE TYPE: No. 5714577e |
| TOPOLOGY: linear |
|
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version 4.5 - 2000 Compugen Ltd GenCore Copyright (c) 1993

- protein search, using sw model OM protein 4, 2002, 14:43:52; Search time 21.66 Seconds (without alignments) 1216.823 Million cell updates/sec April Run on:

....ERRLDAFRAIYNDWRGNGEP 346 1 LRALVFHGNLQYAEIPKSEP... US-09-407-806A-4 346 Title: Perfect score: Sequence:

Gapop 60.0 , Gapext 60.0

OFIGO

Scoring table:

76174552 residues 219241 seqs, 0 Word size Searched:

219241 Total number of hits satisfying chosen parameters

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_68:\* Database :

pir1:\* pir2:\* pir3:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	hypothetical pro	obable phosp	pothetical p	ical pr	pothetical pr	utamate deca	lulase (EC 3.	hosphoprotein ph	served hypoth	58 hypoth	T858 hypothetica	odo	uptake r	ity repress	ori	lation initi	te reducta	pothetical	tica	obable nei	tical	chetical pr	>	yrase/recomb	ihy	ypothetical prot	Уа	ophantRNA	þaþ
SUMMAKIES	ID	7114	5444	7533	H75219	7120	8678	0158	4711	8153	7200	8661	4733	8680	PBPF	6951	4007	3499	6446	8386	7098	7513	145	7240	0969	274	730	327	YWBS	S
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ď	Query	س	•	•	2.3	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	٠	•	•	•
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	apoptosis inhibito	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	monooxygenase 1 [i	probable membrane	hypothetical prote	ATP-dependent RNA	hypothetical prote	pregnancy-specific	probable exodeoxyr	major facilitator	probable ABC-type
571		S61636	T19866	T00792	B96522	D70475	T51603	S50981	T28180	S73545	A64931	176668	B71489	E70391	T36524
7	7	7	7	7	7	7	7	N	7	~	7	7	~	7	7
352	358	365	374	380	389	392	397	430	437	450		475	496	511	539
2.0	•					•			•				•		•
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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hypothetical protein PH0368 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 08-Sep-2000
C;Accession: E71144
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Somerial of the sequence and gene organization of the genome of a hyper-thermophil on the complete sequence and gene organization of the genome of a hyper-thermophil of the ference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:93344137
A;Reference number: B7144
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-364 <KAW>
A;Cross-references: GB:AP000002; NID:93236129; PIDN:BAA29442.1; PID:d1030385; PID:g3:A;Reperimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa;Genetics:
A;Genetics:
A;Gene: PH0368
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0368

Gaps .; 0 Length 364; Indels Score 12; DB 2; Losted. No. 0.00071; 0; Mismatches 0; 3.5%; Sc. larity 100.0%; P. Conservative 0; Local Similarity es 12; Conser Query Match Best Local S Matches 12

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qq δ

## RESULT A64445

probable phosphoesterase (EC 3.1...) MJ1162 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Ju1-2000 C;Accession: A64445 
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blah S;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blah S;Science 273, 1058-1073, 1996 
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasch; Reference number: A64300; MUID:96337999 
A;Reference number: A64445 
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown A;Molocule type: DNA A;Residues: 1-218 <BUL>A;Cross-references: GB:U67558; GB:L77117; NID:91591786; PIDN:AAB99164.1; PID:91591788; C;Genetics: A;Map position: REV1103956-1103300

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A; Obfuku, Y.; Funahashi, T.; Tanaka, T.; Kudon, I.; Lamazani, C.; DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophili A; Reference number: A71000; MUID:98344137
A; Accession: A71203
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-272 <KAW>
Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA31016.1; PID:g3258333
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBa C; Genetics:
A; Genetics:
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A; Geneticanily: Pyrococcus abyssi hypothetical protein PAB2165
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C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
C; Accession: A71203
R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto,
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, I
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cellulase (EC 3.2.1.4) F16B22.6 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01584; B84880
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A.; Yamada, M.; Yasuda
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brary, June 1996
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S75330
hypothetical protein sll1570 - Synechocystis sp. (strain PCC 6803)
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Ju C; Accession: S75330
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamurë o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobact S.
A; Reference number: S74322; MUID:97061201
A; Accession: S75330
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Status: nucleotide sequence was submitted to the EMBL Data Librar C; Genetics:
A; Start codon: GTG
C; Superfamily: Synechocystis hypothetical protein sll1570
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C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-C; Accession: H75219
R; anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into arc A; Reference number: A75001
A; Accession: H75219
A; Accession: H75219
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-272 < KAW>
A; Cross-references: GB: AJ248283; GB: AL096836; NID: g5457433; PIDN: CA
                                                                                                                                                                                                                                                                                                              6803)
C;Superfamily: probable phosphoesterase MTH1882; phosphoesterase C;Keywords: hydrolase F;2-67/Domain: phosphoesterase core homology <PEC>
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C; Genetics:
A; Gene: PAB2165
C; Superfamily: Pyrococcus abyssi hypothetical protein PAB2165
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Superfamily: Synechocystis hypothetical protein s111570
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Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
A; Reference number: A81500; MUID: 20150255
A; Reference number: A81500; MUID: 20150255
A; Accession: F81532
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-619 <REA>
A; Residues: 1-619 <REA>
A; Cross-references: GB: AE002243; GB: AE002161; NID: 97189750; PIDN: AAF38630.1; PID: 9718
A; Experimental source: strain AR39, HL cells
C; Genetics:
A; Genetics:
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A;Experimental source: strain CWL029
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C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C; Accession: F72006
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; CNature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID: 99206606
A; Accession: F72006
A; Accession: F72006
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0; Mismatches
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A; Residues: 1-619 <ARN>
A; Cross-references: GB:
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A;Gene: CP
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Umayam, L.; Tallon, L.
Fraser, C.M.; Venter, C.
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|X
                         R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence.
A;Reference number: 214284
A;Accession: T01584
A;Accession: T01584
A;Restues: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1492 <ROUD
A;Restues: translated from GB/EMBL/DDBJ
A;Residues: 1492 <ROUD
A;Coss references: EMBL:AC003672; NID:g3341671; PID:g3341677
A;Experimental source: cultivar Columbia
A;Residues: 1492 <ROUD
A;Coss references: EMBL:AC003672; NID:g3341677; PID:g3341677
A;Experimental source: cultivar Columbia
A;Tle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A;Reference number: A84420; MUID:20083487
A;Accession: B84880
A;Accession: B84880
A;Accession: B84880
A;Accession: B84880
A;Residues: 1492 <STO>
A;Residues: 1492 <STO>
A;Gene: At2944570; F16B22.6
A;Gene: At2944570; F16B22.6
A;Accession: 74/3; 292/3; 387/3
A;Introns: 74/3; 292/3; 387/3
A;Introns: 74/3; Arabidopsis membrane-anchored cellulase KOR
C;Superfamily: Arabidopsis membrane-anchored cellulase KOR
C;Reywords: glycosldase; hydrolase; polyysaccharide degradation
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C; Species: Homo sapiens (man)
C; Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 08-Oct-1999
C; Accession: A47114
R; Hendrix, P.; Mayer-Jaekel, R.E.; Cron, P.; Goris, J.; Hofsteenge, J.; Merlevede, J. Biol. Chem. 268, 15267-15276, 1993
A; Title: Structure and expression of a 72-kDa regulatory subunit of protein phospha A; Reference number: A47114
A; Reference number: A47114
A; Reference number: A47114
A; Residues: preliminary
A; Molecule type: mRNA
A; Residues: 1-529 < HEN>
A; Residues: 1-529 < HEN>
A; Cross-references: GB:L12146; NID:g190221; PIDN:AAB02614.1; PID:g190222
C; Keywords: alternative splicing; phosphoric monoester hydrolase
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_chang
C;Accession: F81532
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, C.;
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Pred. No. 11;
0; Mismatches
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Mismatches
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100.0%; Pr
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Conservative 0;
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8; Conser
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292 KLVFEGKV
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Best Local
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CT858 hypothetical protein [imported] - Chlamydophila pneumoniae (strain J138)

C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C; Accession: E86617
R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; R; Shirai. Secondarison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349
A; Reference number: B66417
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-619 <STO>
A; Cross-references: GB:BA000008; NID:g8979389; PIDN:BAA99223.1; GSPDB:GN00142
A; Experimental source: strain J138
C; Genetics:
A; Genetics:
A; Genetics:
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A;Title: Nucleotide sequence and mutational analysis of an immunity repressor gene fr. A;Recession: A93579; MUID:85297750
A;Recession: A93579
A;Recession: A93579; MUID:85297750
A;Rocession: A93579; MUID:85297750
A;Releas: 1-147 CDHA
A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophag, A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophag, A;Reference number: A91535; MUID:86056972
A;Title: Nucleotide sequence of the immunity region of Bacillus subtilis bacteriophag, A;Recession: A91535
A;Reference number: A91535; MUID:86056972
A;Reference number: A91535; MUID:86283656
A;Title: Interaction of the Bacillus subtilis phage phil05 repressor with operator DN A;Reference number: S02459; MUID:88283656
A;Title: Interaction of the Bacillus subtilis phage phil05 repressor with operator DN A;Reference number: S02459; MUID:86283656
A;Status: not compared with conceptual translation
A;Residues: A-147 <AND>
A;Reference number: S12688
A;Reference number: Z1688
A;Residues: 4-147 <KOB>
A;Residues: A-147 <KOB
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C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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C;Superfamily: phage phi-105 immunity repressor pro
C;Keywords: DNA binding; early protein; repressor;
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                             C; Species: Erwinia carotovora
C; Species: Erwinia carotovora
C; Date: 23-Nov-1994 #sequence_revision 03-Aug-1995 #text_change 16-Jul-1999.
C; Accession: $47332
R; Rosanas, A.
Submitted to the EMBL Data Library, August 1994
A; Reference number: $47332
A; Residues: 1-878 < ROS>
A; Cross-references: EMBL: X80798; NID: 9525201; PIDN: CAA56777.1; PID: 9525202
A; Cross-references: EMBL: X80798; NID: 9525201; PIDN: CAA56777.1; PID: 9525202
C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase
C; Keywords: ATP; isomerase
F; 1-238/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology < T4T
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C;Species: Bacillus phage phi-105
A;Note: host Bacillus subtilis
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16:
C;Accession: A93579; A91535; S02459; T13543; A24339; A24521
R;Dhaese, P.; Seurinck, J.; De Smet, B.; Van Montagu, M.
Nucleic Acids Res. 13, 5441-5455, 1985
                        Indels
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Mismatches
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Pred. No.
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100.0%; P<sub>J</sub>
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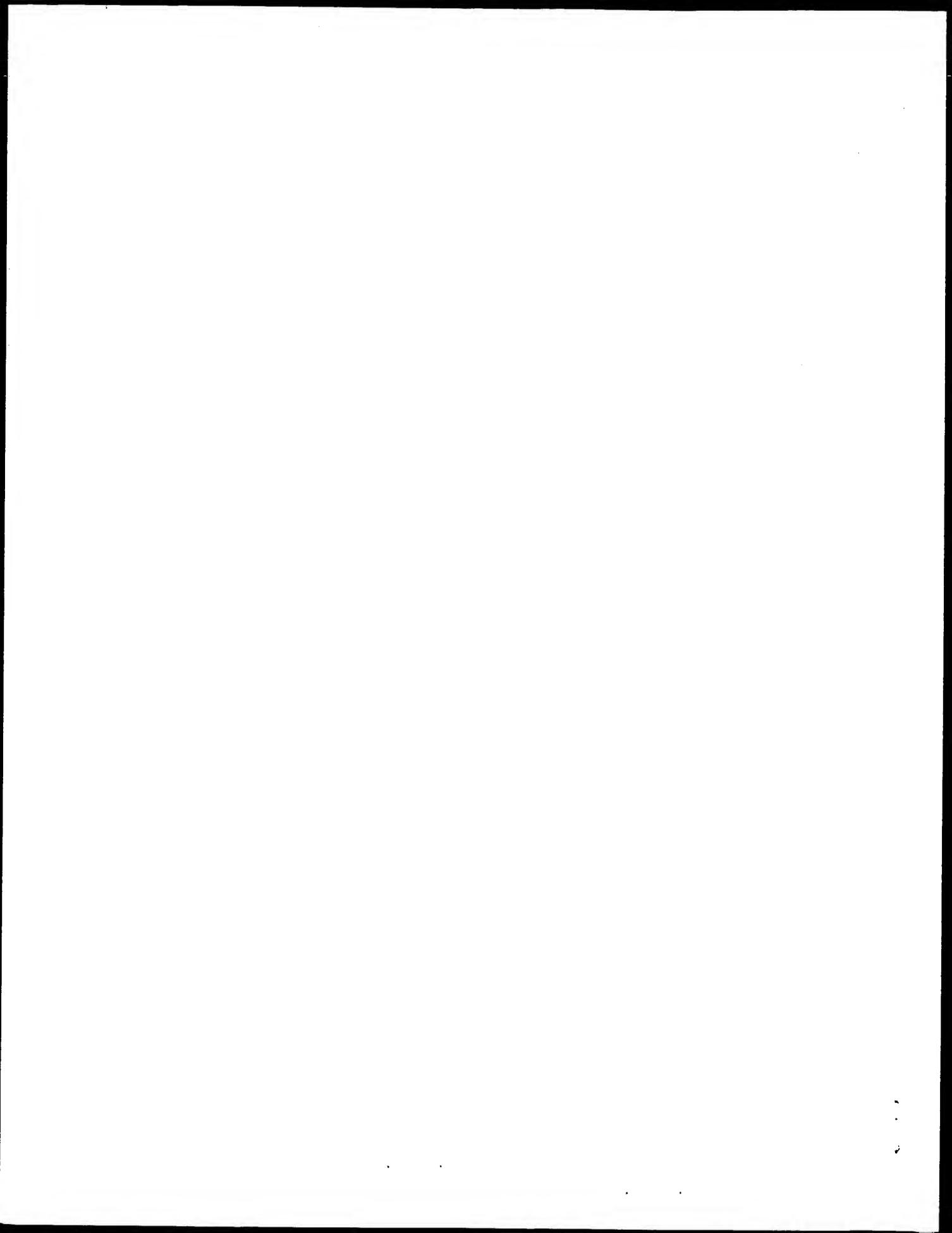
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Search completed: April 4, 2002, 14:46:37 Job time: 165 sec





GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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36664827 residues 100059 seqs, Searched:

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Total number of hits satisfying chosen parameters

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_39:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Q9z6p3 chlamydia	1513 erwinia	06153 ba	9z3q1 rhizobiu	46243 bu	58733 methanococ	55562	96902 my	9per5	9wy77 therm	6 bacillus	58187 ricketts	58186 ricke	21656 bacillus	14438 ustilago	62640 sus	75172 my	38778 sacchar	o 09	76205	3998	38339	0125 micrococ	92834 homo sap	10394 dr	jxk	08169 bos taur	151	0427 rattus n	37462 salmonell	12100 austrolyc	2101 austroly	Q9knz2 vibrio chol
	ID	YA16_CHLP	GYRA_ERWCA	_ 	SYB2_RHIME	IF3_BUCAP	ME	Y4MC_RHISN	END8_MYCTU		MRAY_THEMA	CODV_BACSU	LPXK_RICRI	LPXK_RICMO	SYW_BACSU	GBA3_USTHO		- 1	SMF2_YEAST	- 1	- 1	- 1	- 1	UVRB_MICLU	RPGR_HUMAN	POL4_DROME	PUR4_NEIMB	MPRI_BOVIN	E1_HU	_RA	B_SAL	AUSB	P2_AUS	RL29_VIBCH
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RL29_HALMA	CH10_THEBR	YNC8_YEAST	QACG_STASP	GLNB_PORPU	Y493_HAEIN	RS6_PASMU	C562_ECOLI	RS6_THEMA	EXBD_HAEDU	YBB2_YEAST	ANP3_RHIDE
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### ALIGNMENTS

YA16_CHLPN ID YA16_C AC A
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trictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENZYME FORMS AN A2B2 TETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 161:11-14(1995).

Gene 161:11-14(1995).

-!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA INCLUDING CATENANES AND KNOTTED RINGS.

-!- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95369719; PubMed=7642123; Rosanas A., Barbe J., Gibert I.; "Cloning and sequencing of the gyrA gene from the plant pathogen Erwinia carotovora.";
                                                                                                                                                                                                                                                                                                                    carotovora.
1; Proteobactería; gamma subdivision; Enterobacteriaceae;
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EMBL; X80798; CAA56777.1; -.

InterPro; IPR002205; DNA_topoisoIV.

Pfam; PF00521; DNA_topoisoIV; 1.

R SMART; SM00434; TOP4c; 1.

SMART; SM00434; TOP4c; 1.

"Annisomerase; Isomerase; DNA-binding.

"Annisomerase; Isomerase; DNA-binding.

"Annisomerase; Isomerase; DNA-binding.

"Annisomerase; Isomerase; DNA-binding.

"Annisomerase; Isomerase; DNA-binding.
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red. No. 5;
Mismatches
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01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation updat
DNA GYRASE SUBUNIT A (EC 5.99.1.3).
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InterPro; IPR000178; IF2.
InterPro; IPR003581; TSPc.
ProDom; PD186100; IF2; 1.
SMART; SM00245; TSPc; 1.
Hypothetical protein; Complete proteome.
CONFLICT 619 619 L -> S (IN I
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P41513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dhaese P., Seurinck J., de Smet B., van Montagu M.; "Nucleotide sequence and mutational analysis of an immunity repressor gene from Bacillus subtilis temperate phage phi 105."; Nucleic Acids Res. 13:5441-5455(1985).
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                                                                                                                                                                                                                                                                                                                                                                        van Kaer L., Gansemans Y., van Montagu M., Dhaese P.; "Interaction of the Bacillus subtilis phage phi 105 repressor DNA:
                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
NCBI_TaxID=10717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=86056972; PubMed=3934047;
Cully D.F., Garro A.J.;
"Nucleotide sequence of the immunity region of Bacillus subtilis
bacteriophage phi 105: identification of the repressor gene and its
mRNA and protein products.";
Gene 38:153-164(1985).
-!- SIMILARITY: BELONGS TO THE PBSX(XRE) FAMILY OF TRANSCRIPTIONAL
REGULATORS.
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InterPro; IPRU0130,
Pfam; PF01381; HTH_3; 1.
SMART; SM00530; HTH_XRE; 1.
SMART; SM00530; HTH_XRE; 1.
Transcription regulation; Repressor; DNA-binding; Early
Transcription regulation; Repressor; DNA-binding; Early
Transcription 18 37 H-T-H MOTIF (POTENTIAL).
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                                                  01-JAN-1988 (Rel. 06, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
IMMUNITY REPRESSOR PROTEIN.
Bacteriophage phi-105.
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Mismatches
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(Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. MEDLINE=88283656; PubMed=3135184;
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EMBL; M11920; AAA88396.1; -.
PIR; A24339; RPBPF5.
PIR; S02459; S02459.
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Best Local Similarity 100.0%; F
Matches 7; Conservative 0;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              genetic analysis.";
EMBO J. 7:859-866(1988).
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01-JAN-1988 (Re
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Q9Z3Q1;
30-MAY-2000
30-MAY-2000
RPC_BPPH1
P06153; P.
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SEQUENCE
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"Aromatic amino acid biosynthesis in Buchnera aphidicola (endosymbiont of aphids): cloning and sequencing of a DNA fragment containing aroH-thrS-infC-rpmI-rplT.";

Curr. Microbiol. 30:313-316(1995).

-!- FUNCTION: IF-3 BINDS TO THE 30S RIBOSOMAL SUBUNIT AND SHIFTS THE EQUILIBRUM BETWEEN 70S RIBOSOMES AND THEIR 50S AND 30S SUBUNITS IN FAVOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 30S SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.

-!- SUBUNIT: MONOMER (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       00
                                                                                                                                                                                                                                                           Becker A.;
"The eff-482 locus of Sinorhizobium meliloti CXM1-105 that influences symbiotic effectiveness consists of three genes encoding an endoglycanase, a transcriptional regulator and an adenylate cyclase."; Mol. Gen. Genet. 261:1032-1044(1999).
-!- FUNCTION: SEEMS TO AFFECT THE TRANSCRIPTION OF CYA3. MAY BE NEGATIVELY AUTOREGULATED.
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                                             Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Sinorhizobium.
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Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ225896; CAB38102.1; -.
Nodulation; Transcription regulation; Repressor;
SEQUENCE 151 AA; 16694 MW; 08A85DC217812BFC (
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                                                                                                                                                                                                                                         Simarov
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Pred. No. 15;
0; Mismatches
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01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSLATION INITIATION FACTOR IF-3.
  update)
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20-AUG-2001 (Rel. 40, Last annotation up. PROBABLE TRANSCRIPTIONAL REGULATOR SYRB2
                                                                                                                                                                                                                                      S.N., Keller M.,
                                                                                                                                                                                               STRAIN=CXM1-105;
MEDLINE=99413305; PubMed=10485295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=95245268; PubMed=7766160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conser
                                                                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79
                                                                                                                                      NCBI_TaxID=382;
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EGKVTLK
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P46243;
01-NOV-1995
01-NOV-1995
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                                          SYRB2
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

A Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

A Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

A Noverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

A Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                    n no way commercial
                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
There are no restrictions on it is as its content is in no red. Head, Head,
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Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                       InterPro; 1PRUVILLE 1.

Pfam; PF00707; IF3; 1.

ProDom; PD002880; IF3; 1.

PROSITE; PS00938; IF3; 1.

Initiation factor; Protein biosynthesis.

Initiation factor; Protein biosynthesis.

Initiation factor; Protein biosynthesis.

(BY SIMILARITY).

(BY SIMILARITY).
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231 AA; 25674 MW; 203926DBCD472FAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                  9365C9D6512B1A3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
               between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YD37_METJA STANDARD; PRT; 231 AA. 058733; 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%;
100.0%;
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TIGR; MJ1337; -.
                                                                                                                                            EMBL; U11066; AAC43606.1;
HSSP; P02999; 2IFE.
InterPro; IPR001288; IF3.
Pfam: PF00707; IF3; 1.
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Les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                       178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 LRELRKA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanococcus.
NCBI_TaxID=2190;
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39 LRELRKA 45
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SEQUENCE FROM N.A
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Q9PER5;
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SEQUENCE
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Matches
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                       Gaps
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                                                                                                                                                                                                                                                                                                                                           in
                                                                                                                                                                                               roup;
                                                                                                                                                                                                                                                                                                                                                   for
                                                                                                                                                                                                                                                                   "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycoba
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosen
                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMI the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
                                                                                                                                                                             Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Rhizobium.
    Length 231;
                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN Y4MC F5AA67D9EB7BFB5B CRC64;
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0
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0
                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN Y4MC PRECURSOR.
 DB 1;
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red. No. 23;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).
NEI OR RV3297 OR MT3396 OR MTCY71.37.
Mycobacterium tuberculosis.
Score 7; DB 1; Pred. No. 22; 0; Mismatches
            22;
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                                                                                                                                                                                                                                                                                                                                                                                              1; Signal.
POTENTIAL.
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STRAIN=H37RV;
MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                        (strain NGR234).
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26205 MW;
                                                                                                                                                                                                                                                                                                                                                                                              Plasmid;
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 2.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000085; AAB91766.1;
Hypothetical protein; Plasm:
SIGNAL
                   Conservative
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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        Similarity 7; Conserv
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237 AA;
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les 7; Conserv
                                               GELAFLA 315
                                                                                                                                                                                                   Rhizobiaceae; R
NCBI_TaxID=394;
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                                                                                                                                                                         sp.
                                                                                                      Y4MC_RHISN
P55562;
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Query Match
Best Local
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                                     309
                  Matches
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                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delcher A., Utterback T., welumman C.,
Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA N-GLYCOSYLASE WITH AN AP LYASE ACTIVITY. REQUIRED FOR THE REPAIR OF OXIDATIVE DNA DAMAGE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FPG FAMILY.
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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Xylella fastidiosa.
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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PROSITE; PS01242; FPG; 1.
DNA repair; Hydrolase; Glycosidase; Endonuclease; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
2C97B16CD7CD4002 CRC64;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; ALCOLO TIGR; MT3396; -.
TIGR; MT3396; -.
Tuberculist; Rv3297; -.
InterPro; IPR000191; Fapy_DNA_glyco.
InterPro; IPR000214; Fapy_DNAglyco_zn.
InterPro; IPR01149; Fapy_DNA_glyco; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.0%; Scu
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28525 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z92771; CAB07061.1; -
EMBL; AE007148; AAK47739.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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255 AA;
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Les 7; Conserver
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NCBI_TaxID=2371;
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 FROM ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                      Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
"The genome sequence of the plant pathogen Xylella fastidiosa.";
Nature 406:151-159(2000).
-!- CATALYTIC ACTIVITY: L-ASPARTATE 4-SEMIALDEHYDE + PYRUVATE =
DIHYDRODIPICOLINATE + 2 H(2)0.
-!- PATHWAY: BIOSYNTHESIS OF DIAMINOPIMELATE AND LYSINE FROM ASP.
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PROSITE; PS00665; DHDPS_1; 1.
Lyase; Diaminopimelate biosynthesis; Lysine biosynthesis; Complete proteome.
ACT_SITE 162 162 BY SIMITABLE.
SEQUENCE 302 AA. 215.
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                                                                                                                                                                                                                                                                                                                                                                                               SEMIALDEHYDE; FIRST STEP.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
SIMILARITY: BELONGS TO THE DHDPS FAMILY.
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larity 100.0%; I
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Best Local Similarity
Matches 7: Conser
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STRAIN=9A5C;
MEDLINE=20365717;
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN=MSB8 / DSM 3109;

X MEDLINE=99287316; PubMed=10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

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A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

B Haft D.H., Hickey E.K., Peterson J.D., Nelson D.,

B Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

B Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;

B Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;

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B Heidelberg J., Smith H.O., Venter J.C., Fraser J.C., Fraser J.C., Fraser J.C., White O., White O
                                                                                                                                                                                                                                                                                                                                                                                                                                          and Bacteria from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 4. MRAY
                                              2.7.8.13) (UDP
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC
MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE).
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Pred. No
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Pfam; PF00953; Glycos_transf_4; 1.

PROSITE; PS01347; MRAY_1; 1.

PROSITE; PS01348; MRAY_2; 1.

Peptidoglycan synthesis; Cell division
                                                                                                                           Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
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REMBL; U13634; AAB03369.1; -..

REMBL; U13634; AAB03369.1; -..

REMBL; Z99112; CAA04424.1; -..

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REMBL; Z99112; CAB1487.1; -
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Foulger D., Errington J.;

"Cloning and sequencing 7.5Kbp of DNA from Bacillus subtilis of the codv gene.";

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                                                                        Slack F.J., Serror P., Joyce E., Sonensheln A.L.; "A gene required for nutritional repression of the Bacillus dipeptide permease operon."; Mol. Microbiol. 15:689-702(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia. NCBI_TaxID=783; [1] SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TETRAACYLDISACCHARIDE 4'-KINASE (EC 2.7.1.130) (LIPID A
                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE INTEGRASE/RECOMBINASE CODV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7;
                                                                                                                                                                                                                                                                       STRAIN=168 / JH642;
MEDLINE=95302982; PubMed=7783641;
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-85 FROM N.A. STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rickettsia rickettsii
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tes 7; Conser
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Submitted (C
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P58187;
20-AUG-2001
                                                                                                                                        Bacillus
                                                                                                                                                                                                                                                     SEQUENCE
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[2]
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commercial
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                 Andersson J.O., Andersson S.G.E.;
"Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";
Mol. Biol. Evol. 18:829-839(2001).
-!- FUNCTION: TRANSFERS THE GAMMA-PHOSPHATE OF ATP TO THE 4'-POSITION
OF A TETRAACYLDISACCHARIDE 1-PHOSPHATE INTERMEDIATE (TERMED DS-1-P) TO FORM TETRAACYLDISACCHARIDE 1,4'-BIS-PHOSPHATE (LIPID IVA)
                                                                                                                                                                                     (BY SIMILARITY).

CATALYTIC ACTIVITY: ATP + 2,3-BIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL-(BETA-D-1,6)-2,3-BIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL BETA-PHOSPHATE = ADP + 2,3,2',3'-TETRAKIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL-1,6-BETA-D-GLUCOSAMINE 1,4'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andersson J.O., Andersson S.G.E.;
Andersson J.O., Andersson S.G.E.;
"Pseudogenes, junk DNA and the dynamics of Rickettsia genomes.";
Mol. Biol. Evol. 18:829-839(2001).
-!- FUNCTION: TRANSFERS THE GAMMA-PHOSPHATE OF ATP TO THE 4'-POSITION
OF A TETRAACYLDISACCHARIDE 1-PHOSPHATE INTERMEDIATE (TERMED DS-1-P) TO FORM TETRAACYLDISACCHARIDE 1,4'-BIS-PHOSPHATE (LIPID IVA)
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CATALYTIC ACTIVITY: ATP + 2,3-BIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL-(BETA-D-1,6)-2,3-BIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL BETA-PHOSPHATE = ADP + 2,3,2',3'-TETRAKIS(3-HYDROXYTETRADECANOYL)-D-GLUCOSAMINYL-1,6-BETA-D-GLUCOSAMINE 1,4
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20-AUG-2001 (Rel. 40, Last annotation update)
TETRAACYLDISACCHARIDE 4'-KINASE (EC 2.7.1.130) (LIPID A 4'-KINASE)
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Ferase; Kinase; Lipid A biosynthesis; Lipid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 321;
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                                                                                                                                                                                                                                                                                                                                                                    STEP.
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                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE LPXK FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Pred. No
MEDLINE=21219194; PubMed=11319266;
                                                                                                                                                                                                                                                                                                                                                      PATHWAY: LIPID A BIOSYNTHESIS;
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MEDLINE=21219194; PubMed=11319266;
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36083 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                             BISPHOSPHATE
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ATP-binding.
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20-AUG-2001
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                                                for commercial ib.ch/announce/
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SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1991 (Rel. 19, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2) (TRYPTOPHAN--TRNA LIGASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89211991; PubMed=3149612; Chow K.C., Wong T.F.; "Cloning and nucleotide sequence of the structural gene coding for Bacillus subtilis tryptophanyl-tRNA synthetase."; Gene 73:537-574(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bernstein
between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s or send an email to license@isb-sib.ch).
                                                                                                               AJ293330; CAC33651.1; -.
Ferase; Kinase; Lipid A biosynthesis; Lipid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-32.
MEDLINE=89174673; PubMed=2494170;
Xu Z.J., Love M.L., Ma L.Y.Y., Blum M., Bronskill P.M., I
Grey A.A., Hofmann T., Camerman N., Wong J.T.F.;
"Tryptophanyl-tRNA synthetase from Bacillus subtilis.
Characterization and role of hydrophobicity in substrate
                                                                                                                                                                                                                           Length 325;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264:4304-4311(1989).
ACTIVITY: ATP + L-TRYPTOPHAN + TRNA(TRP)
                                                                                                                                                             ATP (POTENTIAL).
F59126EC871BD9FB CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                             В 1;
30;
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                                                                                                                                                                                                                             Score 7; DB 1
Pred. No. 30;
0; Mismatches
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InterPro; IPR002305; tRNA-synt_lb.
InterPro; IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Bacillus/Staphylococcus group;
NCBI_TaxID=1423;
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larity 100.0%;
Conservative (
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BG10799;
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                                                                                                                                                                                325 AA;
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                                                                                                                                                                                                                                                                                                GLNITGY 47
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SubtiList; B
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                                                                                                                                Transferase;
ATP-binding.
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P21656;
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                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Genet. 256:426-435(1997).

Gen. Genet. 256:426-435(1997).

FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS MODULATORS OR TRANSDUCERS IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THIS SUBUNIT IS INVOLVED IN CAMP REGULATION AND MORPHOGENESIS. IT IS ESSENTIAL FOR DIMORPHIC SWITCHING IN HAPLOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAMMA)
InterPro; IPR002306; tRNA-synt_trp.
Pfam; PF00579; tRNA-synt_1b; 1.
PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=UH100;
MEDLINE=98055158; PubMed=9393440;
Lichter A., Mills D.;
"Fill, a G-protein alpha-subunit that acts upstream of cAMP and is essential for dimorphic switching in haploid cells of Ustilago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GA)
THE ALPHA CHAIN CONTAINS THE GUANINE NUCLEOTIDE BINDING SITE.
SIMILARITY: BELONGS TO THE G-ALPHA FAMILY.
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InterPro; IPR001019; Gprotein_alpha.

Pfam; PF00503; G-alpha; 1.

PRINTS; PR00318; GPROTEINA.

SMART; SM00275; G-alpha; 1.

GTP-binding; Transducer; Multigene family.

NP_BIND 41 48 GTP (BY SIMILARITY).

NP_BIND 202 206 GTP (BY SIMILARITY).

NP_BIND 271 274 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ustilago hordei (Smut fungus).
Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae;
                                                                                                                                                                                                                                                                                                                                                                                                GBA3_USTHO STANDARD; PRT; 354 AA. 014438; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-3 SUBUNIT.
                                                                                                       "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
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Mismatches
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197
196 A
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Length 354

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DB

7;

Score

2.0%;

Query Match

0; Indels 0; Best Local Similarity 100.0%; Pred. No. 32; Matches 7; Conservative 0; Mismatches

0;

Gaps

115 DPIIPAI 121 |||||||| 135 DPIIPAI 141 δλ

Op

Search completed: April 4, 2002, 14:50:10 Job time: 248 sec

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

model OM protein - protein search, using sw 4, 2002, 14:45:32; Search time 28.85 Seconds (without alignments) 1754.254 Million cell updates/sec April Run on:

.... ERRLDAFRAIYNDWRGNGEP 346 US-09-407-806A-4 346 1 LRALVFHGNLQYAEIPKSEP.... score: Sedneuce: Title: Perfect

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

473505 seqs, 146272329 residues

Searched:

0 Word size 473505

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Database :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description		Q9hhb5 pyrococcus		Q9k2w4 lactococcus	~	8562	321		059526 pyrococcus	_	_	030418 lactococcus	Q9cg20 lactococcus		090992 human immun	008929 mus musculu	Q9cfk0 lactococcus	P96467 streptococc	080190 bacteriopha	Q9avf7 amaranthus
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## ALIGNMENTS

RESULT 1  10 HB15   10 HB2	Pyrococcus.	0; Gaps		Pyrococcus.
HHB5 Q9HHB5 PRELIMINARY; PRT; 364 AA. Q9HHB5 O1-MAR-2001 (TrEMBLrel. 16, Last sequence update) O1-MAR-2001 (TrEMBLrel. 16, Last sequence update) O1-MAR-2001 (TrEMBLrel. 16, Last sequence update) O1-MAR-2001 (TrEMBLrel. 16, Last annotation update) ALPA-GALACTOSIDASE. GALA. Pyrococcus Euryarchaeota; Thermococcales; Thermococcacea Archaea; Buryarchaeota; Thermococcales; Thermococcacea NCBI_TAXID-2261; [1] SEQUENCE FROM N.A. STRAIN=DSM 3638; Verhees C.H.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ database EMBL; AF195244; AAG28455.1; SEQUENCE 364 AA; 41545 MW; 3E8E0AF5BDCCF2A5 CRC64; SEQUENCE 364 AA; 41545 MW		.,		
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TRUNCATED GLUTAMATE DECARBOXYLASE (FRAGMENT).
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01-JUN-2001
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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STRAIN=ML, ATCC19257, 01-1, 924, F-16, AND HP;
MEDLINE=20250682; PubMed=10788408;
Nomura M., Kobayashi M., Ohmomo S., Okamoto T.;
"Inactivation of the glutamate decarboxylase gene in Lactococcus lactis subsp. cremoris.";
                       STRAIN=CV13;

MEDLINE=98344137; PubMed=9679194;

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Na,

Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuk

Hunahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Og

Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

Masuchi Y., Shizuya H., Kikuchi H.;

"Complete sequence and gene organization of the genome of a hy

thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

DNA Res. 5:55-76(1998).

EMBL; AP000002; BAA29442.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 364 AA; 41755 MW; 7B4B36AB4A975BAD CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TRUNCATED GLUTAMATE DECARBOXYLASE.
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Last annotation update)
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100.0%; Pr
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AB03327; BAA95948.1; -.; AB033218; BAA95944.1; -.; AB033219; BAA95946.1; -.; AB033221; BAA95946.1; -.; AB033225; BAA95946.1; -.; AB033225; BAA95947.1; -.
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SEQUENCE FROM N.A.

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Retlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Nerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Noverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Noverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Noverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Noterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Noterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Rienk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus

"Tomplete genome sequence of the methanogenic archaeon, Methanococcus

"EMBL, U67558; AAB99164.1; -.

RIGR; MJ1162; -.

TITTER; MJ1162; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
Lactococcus lactis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                               STRAIN=H-61;
MEDLINE=20250682; PubMed=10788408;
Nomura M., Kobayashi M., Ohmomo S., Okamoto T.;
"Inactivation of the glutamate decarboxylase gene in Lactococcus
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Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                       PPL. Environ. Microbiol. 66:2235-2237(2000).

-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

EMBL; AB033229; BAA95949.1; -.

InterPro; IPR002129; Pyridoxal_dec.

Pfam; PF00282; pyridoxal_dec.

Decarboxylase; Lyase; Pyridoxal phosphate.

SERTIFFICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 105;
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Hypothetical protein; Complete proteome.
SEQUENCE 218 AA; 24676 MW; 2F9D763416039EE4 CRC64;
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on update)
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Last sequence upon Last annotation
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Mismatches
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                                                                                                                                                                                                                                                     lactis subsp. cremoris.";
Appl. Environ. Microbiol.
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les 8; Conser
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SEQUENCE FROM N.A.
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MEDLINE=94150718; PubMed=7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Anderson K., Eavello J., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R11G11.10.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  K., Una
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

EMBL; D90904; BAA17244.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 243 AA; 26620 MW; 37DE109025773501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cyanobacterium
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Kimura T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Hosouchi T., Matsuno A., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 243;
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                                                                                                                                                                                                                                                                      SLL1570.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBI_TaxID=1148;
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                                                                                                                                                                                   (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 14, Last annotation update)
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Last annotation updat
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3%; SCC
100.0%; Pr
0;
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01-FEB-1997 (TrEMBLrel. 02, La
01-JUN-2000 (TrEMBLrel. 14, La
HYPOTHETICAL 26.6 KDA PROTEIN.
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Nature 368:32-38(1994)
                                                                                                                                                PRELIMINARY;
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Best Local Similarity
8; Conserve
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                      10 EVIDELNS 77
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P73217;
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STRAIN=OT3;

MEDLINE=98344137; PubMed=9679194;

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Kawarabayasi Y., Sawada M., Horikawa H., Hosoyama A., Nagai Y.,

Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

R. Sakai M., Ohfuku Y.,

R. Sakai M., Ohfuku Y.,

A Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,

A Aoki K.-I., Shizuya H., Kikuchi H.;

R. Masuchi Y., Shizuya H., Kikuchi H.;

T. Complete sequence and gene organization of the genome of a hyper-

T. Thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

DNA Res. 5:55-76(1998).

EMBL; AP000007; BAA31016.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
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Pfam; PF01336; tRNA_anti; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 272 AA; 31654 MW; 3580BC7EEACCDDBB CRC64;
                                                                                                                                              Waterston R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF022976; AAC69084.1; -
InterPro; IPR000276; GPCR_Rhodpsn.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
STRAIN=BRISTOL N2;
Davidson S., Wohldmann P., Bauer C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09V1Z1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 31.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 31.7 KDA PROTEIN PH1894.
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Pred. No. 13;
; Mismatches
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13;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last seq
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llarity 100.0%; F
Conservative 0;
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                                                                                                       SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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STRAIN=BRISTOL N2;

MEDLINE=94150718; Pubmed=7906398;

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

Raaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                              chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                  Yrococcus
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                "Pyrococcus abyssi genome sequence: insights into archaeal structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248283; CAB49207.1;
InterPro; IPR002309; tRNA-synt_2.
InterPro; IPR002309; tRNA-synt_2.
Pfam; PF01336; tRNA_anti; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 272 AA; 31827 MW; 515DA586372DD837 CRC64;
                            Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 272;
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STRAIN=BRISTOL N2;
Waterston R.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022976; AAC69085.1; -
SEQUENCE 328 AA; 37192 MW; 12339872BA82C5D6 CRC64;
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Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 13;
; Mismatches
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O16953;
O1-JAN-1998 (TrEMBLrel. 05, C1
01-JAN-1998 (TrEMBLrel. 05, L2
01-NOV-1998 (TrEMBLrel. 08, L2
COSMID R11G11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                          STRAIN-ORSAY;
Heilig R.;
"Pyrococcus abyssi
                                                                                                                                  SEQUENCE FROM N.A.
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PAB2165
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RL
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Length 328;

DB 5; 16;

Score 8; DI Pred. No.

2.3%; 100.0%;

Best Local Similarity

Query Match

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Gaps
                                                                                                                                                                                                                                                                                                                     chloride-inducible acid resistance mechanism in Lactococcus lactis
                                                                                                                                                                                                                                                                                                                                                                                            Nomura M., Fujita Y., Kobayashi M., Oomomo S.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES

THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE.

-!- CATALYTIC ACTIVITY: L-GLUTAMATE = 4-AMINOBUTANOATE + CO(2).

-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-!- INDUCTION: EXPRESSION IS HIGHEST AT ONSET OF STATIONARY PHASE IN PRESENCE OF NACL AND GLUTAMATE, AND AT LOW PH. CHLORIDE-DEPENDENT EXPRESSION IS ACTIVATED BY GADR.

-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
                                                                                                                                                                                         Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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28B94EB3FEEB168D CRC64;
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Last annotation update)
4.1.1.15).
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Pred. No. 22;
0; Mismatches
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its regulation.";
....rohiol. 27:299-310(1998).
                                                                                                                                                                                                                                                                  STRAIN=MG1363;
MEDLINE=98143417; PubMed=9484886;
Sanders J.W., Leenhouts K., Burgh
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100.0%; P
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                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17, GLUTAMATE DECARBOXYLASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53849 MW;
                                                                                                      PRELIMINARY;
                                                                                                                          01-JAN-1998 (TrEMBLrel. 01-JAN-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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|140 LLLRELRK 147
             170 LLLRELRK 177
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8; Conserv
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O30418; O50645;
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100.0%;

Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                   coccaceae;
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Genome Res. 0:0-0(2001).

-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-!- SIMILARITY: PYRIDOXAL-DEPENDENT DECARBOXYLASE FAMILY.

EMBL; AE006361; AAK05388.1; -.

InterPro; IPR002129; Pyridoxal_deC.

Pfam; PF00282; pyridoxal_deC; 1.

Complete proteome; Decarboxylase; Lyase; Pyridoxal phosphate.

SEQUENCE 466 AA; 53926 MW; BCDC732253E473C2 CRC64;
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SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L..
Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Adé
Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adé
Somerville C.R., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC F16B22 genomic s'
"Arabidopsis thaliana chromosome II BAC F16B22 genomic s'
submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
FWRI.: AC003672; AAC27459.1; -.
                                                                                                                                                                                            lactis).
Streptod
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on update)
                                                                                                   Last sequence update)
Last annotation update)
4.1.1.15).
                                                                                                                                                                                            Lactococcus lactis (subsp. lactis) (Streptococcus Bacteria; Firmicutes; Bacillus/Clostridium group;
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; Pred. No. 22;
0; Mismatches
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01-NOV-1998 (TrEMBLrel. 08, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
PUTATIVE GLYCOSYL HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mendel; 31158; Arath;1057;31158.
InterPro; IPR001701; Glyco_hydro_9.
Pfam; PF00759; Glyco_hydro_9; 1.
PROSITE; PS00592; GLYCOSYL_HYDROL_F9_1; 1.
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
GLUTAMATE DECARBOXYLASE
                                       PRELIMINARY;
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nes 8; Conser
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NCBL_TaxID=3702;
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Query Match

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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=V11267;
STRAIN=V11267;
Heyndrickx L., Janssens W., Coppens S., Vereecken K., Willems B., Fransen K., Colebunders R., Vandenbruaene M., Van Der Groen G.;
"HIV-1 C2V3 env diversity among Belgian individuals.";
"HIV-1 C2V3 env diversity among Belgian individuals.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ228225; CAA12855.1; -.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
NON_TER 85 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 04, Created)
(TrEMBLrel. 04, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                        (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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STRAIN=BALB/C; TISSUE=LIVER;
Zimmermann W., Fischer B., Olsen A., Nedellec Submitted (JUN-1997) to the EMBL/GenBank/DDBJ EMBL; Y13561; CAA73896.1; -.
InterPro; IPR003599; Ig.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
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Mismatches
Pred. No. 23
Mismatches
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100.0%;
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9453 MW;
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              Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                             090992;
01-NOV-1998 (TrEMBI
01-NOV-1998 (TrEMBI
01-JUN-2001 (TrEMBI
GP120 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AA;
                                                                 292 KLVFEGKV 299
                                        180 KLVFEGKV 187
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01-JUL-1997
01-JUL-1997
01-JUN-2001
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0; Gaps 0; Indels 0; Mismatches 7; Conservative Matches

0;

270 LKHSGRE 276 |||||||||| 70 LKHSGRE 76 Qγ

QQ

Search completed: April 4, 2002, 14:49:45 Job time: 253 sec

4.5 Compugen Ltd. version - 2000 GenCore Copyright (c) 1993

model S using - protein search, OM protein

Seconds 25.56 Search time 2002, 14:34:16 4 April Run on:

ts) cell updates/sec (without alignmen 1002.714 Million

Title:

.ERRLDAFRAIYNDWRGNGEP 346 LRALVFHGNLQYAEIPKSEP US-09-407-806A-4 1778 1 LRALVFHGNI.OYAFT score: Sequence: Perfect

0.5 Gapext BLOSUM62 Gapop 10.0 Scoring table:

74073290 residues 522463 seqs, Searched:

522463 hits satisfying chosen parameters of number Total

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database

A\_Geneseq\_1101:\*

1: /SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
2: /SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
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13: /SIDS2/gcgdata/geneseq/geneseqp/AA1991.DAT:\*
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17: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
18: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
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28: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:\*
29: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:\*

No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. Pred. No. and is score

#### SUMMARIES

	Description	Thermostable alpha	Pyrococcus furiosu	Super heat resista	S. epidermidis ope	S. epidermidis ope	Protein involved i	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Zea mays protein f	Cotton UDP glucose
	QI	AAW34643	AAR47504	AAW54870	AAG82181	AAG82196	AAY36871	AAG29078	AAG29077	AAG29076	AAG34045	AAR88328
	DB	18	15	19	22	22	20	21	21	21	21	17
	Length DB	364	649	653	434	557	1396	216	218	235	377	465
yp	Query Match	•								5.3		
	Score	œ	•	•		•	•	93.5	93.5	93.5	93	93
	Result No.		7	m	4	5	9	7	∞	δ	10	11

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### ALIGNMENTS

AAW34643 standard; Protein; 364 AA AAW34643 RESULT

AAW34643;

Thermostable alpha-galactosidase AEDII12RA-alpha-gal-18GC.

(first entry)

27-MAR-1998

Alpha-galactosidase; alpha-glycosidase; thermostable enzyme; food processing; alpha glycoside hydrolysis; raffinose; stachyose; verbascose; bean; flatulence; AEDII12RA-alpha-gal-18GC. 

Thermococcus alcaliphilus strain AEDII12RA

Location/Qualifiers /note= "encoded by Misc-difference 329 Key

WO9732974-A1

12-SEP-1997.

97WO-US01452. 05-FEB-1997; 96US-0613220. 08-MAR-1996; (RECO-) RECOMBINANT BIOCATALYSIS INC.

Rudolph MJ; Murphy D, Reid J,

WPI; 1997-470541/43. N-PSDB; AAT93753.

```
thermostable alpha-galactosidase of Thermococcus alcaliphilus

AEDI112RA, a bacterium that shows optimum growth at 85 deg c and
pH 9.5. Also claimed are: (1) an isolated polynucleotide (see
AAT93753) encoding the alpha-galactosidase; (2) a vector containing
the polynucleotide or homologous or complementary sequences; (2)
host cells containing the vector; (3) a process for producing the
alpha-galactosidase in transformed or transfected host cells; an
enzyme showing at least 70% identity to alpha-galactosidase and
comprising at least 70% identity to alpha-galactosidase and
comprising at least 30 amino acid residues of its sequence; and (4)
a method for hydrolysing alpha-galactoside bonds using the enzyme.
The enzyme can be used to hydrolyse raffinose to sucrose and glucose
in sugar beet processing (raffinose inhibits crystallisation of
sucrose), and as a digestive aid to hydrolyse raffinose, stachyose
and verbascose in beans and other gassy foods.
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    from Thermococcus
                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                   to hydrolyse
                                                                                        comprises AEDII12RA-alpha-gal-18GC,
                                                                                                                                                                                                                                                                                                                                                                    Score 1586; DB 18;
Pred. No. 1.4e-150;
L; Mismatches 0;
encoding alpha-glycosidase
- used in food processing t
des, e.g. raffinose
                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                             English
                                                                                                                                                                                                                                                                                                                                                                     89.2%;
illarity 94.8%;
Conservative
                                                          32pp;
                                                                                                                                                                                                                                                                                                                           364 AA;
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les 345; Conser
                              alpha-glycosides,
                                                          1;
 acid
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               alcaliphilus
                                                          1; Fig
                                                                                       protein
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Best Local S
Matches 345
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                                                                                                                                                                                                                                                                                                                            Sequence
                                                          Claim
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21;

Purified Pyrococcus furiosus alpha-amylase - used for tindustrial liquefaction of gluco-polymers at high temps

WPI; 1994-009532/02

92US-0893928

09-JUN-1992;

JOHNS HOPKINS

VINU ( OCYU)

93EP-0303801

17-MAY-1993;

05-JAN-1994

EP577257-A.

Figure 9; 41pp; English.

Claim 2;

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AAW54870;
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Matches
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                                                                                                                                                                                                             649
                                                                                                                                                                                                           standard; protein;
                                                                                                                                                                                                                                                                        thermostable
                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                 furiosus;
                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                    furiosus
                                                                                                                                                                                                                                                                                     Pyrococcus furiosus
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glucopolymers;
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                                                                                                                                                                                                          AAR47504
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Gaps
                                                                                                                                                                                                                                                                                                              The purifed Pyrococcus furiosus alpha amylase can act on substrates with a low degree of polymerisation. e.g. glucose polymers as short as maltotriose. The enzyme can be used for efficient industrial liquefaction of glucopolymers at high temperatures.
                                                                                                                                                                                                                                                                                                                                                                                                        TAILPLLPLSRVEAQVQRDRVKEELFE -- - VSPKGFWLPE-LADPIIPAILKDNGYEYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----AIKPIKPLPHLIKAQREKRFRYISYLLLREL
                                                                                                                                                                                                                                                                                   24 EKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIEIIGTS-Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 RKAIKLVF-----EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Super heat-resistant 4-alpha-glucanotransferase; heat-treatment; alpha-1,4-glucan; alpha-1,4-glucoside bond.
                                                                                                                                                                                           Length 649;
                                                                                                                                                                                                                                             131;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                      DB 15;
                                                                                                                                                                                                                       52;
117;
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                                                                                                                                                                                      118.5; DB 6.7%; Score 118.5; DB 120.2%; Pred. No. 0.0052 Conservative 64; Mismatches 1
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19;
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                                                                                                                                                                                                             nseq
                                                                                                                                                                                                                                                                                                                                                                                                                            115;
                                                                                                                                                                                                                                                                                                                                                                                                   653;
                                                                                                                                                                                                            New 4-alpha-glucanotransferase which has been heat-treated
high temperatures to transfer at least one glucose unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reading frame protein sequence SEQ ID
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--deklryl-
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                                                                                                                                                                                                                                                                                                                                                                                                                           127;
                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 100.5; Dilarity 19.3%; Pred. No. 0.33; Conservative 67; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ktleylhslddgdeskvavfhddgekfgvwpg-
                                                                                                                                                                                                                                                    Claim 4; Page 10-13; 18pp; Japanese.
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                                                                                                                                         SEIKAGAKU KOGYO KK
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                                                                           96JP-0311117
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N-PSDB; AAV27026.
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Best Local Similarity
Matches 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAMLFSAHLNS-
                                                                                                                                                                                                                                                                                                                                                           653 AA;
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                                                                                                                              (BEAB-) BE ABLE
(NAGA-) NAGASE
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Pyrococcus sp
                        JP10150986-A
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                                                 09-JUN-1998
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides may also be used to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA colymcleotide sequences from the present invention. AAH55091 to AAH55090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271
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                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding polypeptides from Staphylococcus epidermidis useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPK-----GFWLPELADPIIPAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 AEIPKSE-PKVIEKAYIPVIETLIKEEPFGLNITGYTLKFLPKD---IILVKGGIASDLI
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diagnosis;
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strain; infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.5%; Score 97.5; DB 22.4%; Pred. No. 0.37; ive 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pseisrkdevw-egesglltiaggkltgyrhma----
                                                                                                                                                                                                                                                                                                                                                                                                English.
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 SR1
                                                                                                                                                                                       99US-0164258.
                                                                                                                                                                                                                                                                                                                                                                                                2188pp;
                                                                                                                                                      2000WO-US30782
                                                  epidermidis.
Staphylococcus epidermidis vaccination; endocarditis.
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                                                                                                                                                                                                                                                                                                                                                                                                   411;
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                                                                                                                                                                                                                                                                                                              N-PSDB; AAH53031
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page
                                                   Staphylococcus
                                                                                     WO200134809-A2
                                                                                                                                                                                                                        ) GLAXO
                                                                                                                                                        09-NOV-2000;
                                                                                                                                                                                       09-NOV-1999;
                                                                                                                                                                                                                                                              Kimmerly WJ;
                                                                                                                     17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81;
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may then be
the bacteria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of the activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the avammalification of the present invention.
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idermidis.
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 447 no sequences are present for SEQ ID NO:4465 to 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids encoding polypeptides from Staphylococcus epidermidis
or vaccinating against infections, e.g. endocarditis -
                                              edvarr
                                                                                                                                                                                                                                                                                                                                                                NO:1486
       Ŧ
GRELYLRTSSWADKSLRIWREDEGNARLNMLYNMRGELAFLAENSD-ARGWPLP
                    272 kqeyglkfescatknlkisggdvggsk-nfeh-----fveqkvdaakgfgid
                                                                                                                                                                                                                                                                                                                                                                                                     us epidermidis SR1 strain; infection; diagnosis endocarditis.
                                                                                                                                                                                                                                                                                                                                                          epidermidis open reading frame protein sequence SEQ ID
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                                                                                                                                                                                                                                AAG82196 standard; Protein; 557 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 420-421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-316495/33
N-PSDB; AAH53046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                557 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus vaccination; er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-2000;
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274
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16;

Gaps

Indels

142;

Length 557

DB 22;

Score 97.5; DB Pred. No. 0.53; 3; Mismatches

th 5.5%; So Similarity 22.4%; P181; Conservative 53;

Query Match Best Local

Matches

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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                          agvkkserkkmlskqetlnkeplvkrd--glkgggyyveyrtddarltievmkkaaenga
    --IILVKGGIASDLI
                                                                   --GFWLPELADPIIPAIL
                                                                                                                                                            --rsgdyarnnkqlrltkgvhvvidqskfplgqavyfdtekdgrmi-faipregkayvgt
                                                                                                                                                                                              ---LRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRL
                                                                                                                                                                                                                           tdtfydnekatplttqedrdylinainymfp---tvnvkdediestwagirplilekgkd
                                                                                                                                                                                                                                                          PLMNPKKVASWIEDKNILLYGTDIEFIGYRDIAGRMSVEGLLEVIDELNSELCPSELKHS
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                                                                                                                              KDNGYEYLFADEAMLFSAHLNSAIKPIK-PLPHLIKAQREKRFRYISYLLLRE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intermediate metabolism of polypeptides.
                                                                                            eiinytksehftydsnkkvngievldmidgetyaikakkvinasgpwvdev---
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---leivdll
AEIPKSE-PKVIEKAYIPVIETLIKEEPFGLNITGYTLKFLPKD-
                                                              EIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPK--
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                                                                                                                                                                                                                                                                                                                                         :| |: | |:|| | ::| :| 395 kqeyglkfescatknlkisggdvggsk-nfeh----
                                                                                                                                                                                                                                                                                         pseisrkdevw-egesglltiaggkltgyrhma---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; Protein; 1396 AA
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97FR-0015041.
97FR-0016034.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-371125/31
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28-NOV-1997;
17-DEC-1997;
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18
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promoter;
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        j infants;
invention
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 nongonococcal uretritis, epidymitis, cervicitis, salpingiti perihepatitis, bartholinitis; pneumopathy in breast feeding and venereal lymphogranulomatosis. The polypeptides of the may be of use in treating these diseases.
                                                                                         15 IPKSEPKVIEKAYIPVIETLIKEEPFGLN--ITGYTLKFLPKDIILVKGGIASI
                                                                                                                     73 TSYTA-----ILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPI-I
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                                                                                                                                                                                 LLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAV--
                                                           Score 97.5; Di
Pred. No. 2;
11; Mismatches
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                                                     5.5%; Sc.
22.0%; Pre
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
99US-0127462.
99US-0128234.
99US-0128714.
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termination sequence.
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                                       1396 AA;
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                                                                    Similarity
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
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Best Local
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Matches
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RR 23-APR-1999; 99US-0130449.

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RR 05-MAY-1999; 99US-0132487.

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RR 16-JUN-1999; 99US-013945.

RR 16-JUN-1999; 99US-013945.

RR 18-JUN-1999; 99US-013945.

RR 23-JUN-1999; 99US-013945.

RR 23-
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PR 22-7UC-1999; 99US-015103.
PR 22-7UC-1999; 99US-015103.
PR 23-7UC-1999; 99US-015203.
PR 23-7UC-
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promoter;
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99US-0159637.
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99US-0123180.
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19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 22-JUL-1999; 23-JUL-1999; 24-AUG-1999; 05-AUG-1999; 05-AUG-1999; 05-AUG-1999; 07-AUG-1999; 06-AUG-1999; 07-AUG-1999; 06-AUG-1999; 07-AUG-1999; 06-AUG-1999; 07-AUG-1999; 06-AUG-1999; 07-AUG-1999; 11-AUG-1999; 11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999; 14-AUG-1999; 15-AUG-1999; 16-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 21-AUG-1999; 22-AUG-1999; 22-AUG-1999; 23-AUG-1999; 24-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999;	0 - SEP - 199 3 - SEP - 199 5 - SEP - 199 6 - SEP - 199 0 - SEP - 199 3 - SEP - 199 4 - SEP - 199 9 - SEP - 199 6 - OCT - 199 6 - OCT - 199 7 - OCT - 199 8 - OCT - 199
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promoter;
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hybridisation assay; genetic mapping; gene expression contro
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                                                                                                                                                                                                                                                                                  DB
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Pred. No. 0
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99US-0159320.
99US-0159330.
99US-0159331.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein;
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12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
                                                                                                                                                                                                                                                                               Query Match
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990S-0126264.
990S-01262824.
990S-0127462.
990S-0137522.
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990S-0141842.
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990S-0143542.
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990S-0150884.
990S-0151080.
990S-0151080.
990S-0151303.
990S-0151303.
990S-0151333.
13 - JUL - 1999;

14 - JUL - 1999;

15 - JUL - 1999;

16 - JUL - 1999;

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28 - SEP - 1999;

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28 - SEP - 1999;
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metabolic pathway;
control; promoter;
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expression
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0.37;
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Pred. No. 0.37
4; Mismatches
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990S-0157753.
990S-0157753.
990S-0158029.
990S-0158232.
990S-0159293.
990S-0159294.
990S-0159330.
990S-0159330.
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990S-0159637.
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990S-0160741.
990S-0160768.
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990S-0161409.
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27 ksnnqkrfs-
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04-OCT-1999;
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07-OCT-1999;
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Matches 45
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20-SEP-1999;
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99US-0123180.
99US-0123548.
99US-0125788.
99US-0125788.
99US-0126264.
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99US-013621.
99US-013724.
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99US-013863.
99US-0132485.
99US-0132487.
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99US-0133421.
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99US-0139456.
99US-0139456.
99US-013946.
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                                       2000EP
                                                          25-FEB-1999; 05-MAR-1999; 23-MAR-1999; 23-MAR-1999; 25-MAR-1999; 25-MAR-1999; 25-MAR-1999; 29-MAR-1999; 29-MAR-1999; 29-MAR-1999; 29-MAR-1999; 29-MAR-1999; 23-APR-1999; 23-APR-1999; 24-MAY-1999; 25-MAY-1999; 26-MAY-1999; 27-MAY-1999; 27-MAY-1999; 28-MAY-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 28-JUN-1999; 29-JUN-1999; 29-JU
                                      -2000;
                                     -FEB-
             -SEP
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99US-0142950. 99US-0142390. 99US-0142803. 99US-0142920. 99US-0142977. 99US-0144354. 99US-0144331. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0144332. 99US-0145086. 99US-0145086. 99US-0145086. 99US-0145086. 99US-014519. 99US-0145913. 99US-0145913. 99US-0145913. 99US-0145913. 99US-0145913. 99US-0145913. 99US-0145913. 99US-0145913. 99US-0145913.	US-014/203 US-014/416 US-014/416 US-014/493 US-0148341 US-0148341 US-0148341 US-0148341 US-0149925 US-0149925 US-01499368 US-01499368 US-01499368 US-0149930 US-0149930 US-0151065 US-01510884 US-0151088 US-0151303 US-0151363 US-01533738 US-0153070 US-0153363 US-0153363 US-0153363
PR 02-JUL-1999; PR 06-JUL-1999; PR 08-JUL-1999; PR 12-JUL-1999; PR 12-JUL-1999; PR 13-JUL-1999; PR 14-JUL-1999; PR 19-JUL-1999; PR 19-JUL-1999; PR 19-JUL-1999; PR 19-JUL-1999; PR 20-JUL-1999; PR 20-JUL-1999; PR 21-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 22-JUL-1999; PR 23-JUL-1999; PR 27-JUL-1999; PR 02-AUG-1999; PR 03-AUG-1999; PR 03-AUG-1999; PR 05-AUG-1999;	06-AUG-1999 09-AUG-1999 09-AUG-1999 09-AUG-1999 10-AUG-1999 11-AUG-1999 13-AUG-1999 13-AUG-1999 14-AUG-1999 15-AUG-1999 15-AUG-1999 16-AUG-1999 17-AUG-1999 18-AUG-1999 18-AUG-1999 18-AUG-1999 18-AUG-1999 18-AUG-1999 19-AUG-1999 10-SEP-1999 10-SEP-1999 113-SEP-1999 113-SEP-1999 113-SEP-1999

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Gossypium hirsutum.
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                                         06-JUN-1994;
                                                        06-JUN-1994;
                           19-DEC-1995.
                                                                                                               recombinant
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                                                                                    WPI;
                                                                                                                                                                                                                                      Matches
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aqgkeyvf
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0.84;
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Pred.
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99US-0155139.
99US-0155486.
99US-0155659.
99US-0156596.
99US-0157717.
99US-0157753.
99US-0157765.
99US-0158029.
99US-0158232.
99US-0159293.
99US-0159331.
99US-0159331.
99US-0159638.
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99US-0159638.
99US-0160741.
99US-0160981.
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99US-0160981.
99US-0161404.
99US-0161361.
                                                                                                                                                                                                                                                                                        5.2%;
ilarity 25.3%;
Conservative 2
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59; Conser
 22-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
05-OCT-1999;
07-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    line diphosphate glucose phosphorylase; transgenic plant; glucose phosphorylase; cell wall synthesis; starch biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- DNGYEYLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYISYLLLRELRKAIKLVFEGKVTL--
                                                                                                                                                                                                                                                                                                       The present sequence is that of UDP glucose synthase from cotton. E.coli host cells transformed with a plasmid carrying cDNA coding for this enzyme had UDP glucose synthetic activity of 150 U and UDP glucose decomposition activity of 130 U; this compares with values of 0 and 0.027, respectively for E.coli transformed with a plasmid not carrying the UDP glucose synthase gene.
                                                                                                                                                                                    gootton UDP glucose synthase - also vectors contg. the DNA, useful for prodn. of stable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -KVKDIEAVPV-----WVAVNTAVMLIGRLPLM-----NPKKV 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 iaqvpdehvnefksiekfkifntnnlwvnlnaikrlveadelkmeiipnpkev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --QVQRDRVKEELFEVSP-----KGFWLPELADPIIPAILK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A uridine diphosphate (UDP) glucose phosphorylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53 PKDIILVKGGIA-SDL----IEIIGTSYTAILPLLPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 93;
Pred. No.
                                                                                                                                                                                                                                                                           Claim 2; Page 7-9; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.2%;
94JP-0123788
                                       94JP-0123788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                  (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                          sequence encoding
                                                                                                                                                                                                               microbes
                                                                                                                            1996-072337/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 AA;
                                                                                                                                                AAT03700
                                                                                                                                                                                                                                  glucose synthase
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transgenic her or lower
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              -SRVEA 89
                                                                                                                                                                                                            The present sequence represnets a plant uridine diphosphate (UDP) gphosphorylase. The polynucleotides may be used to create transgenic plants which express the UDP glucose phosphorylase at higher or low levels than normal or in cell types or developmental stages in which they are not normally found. This would alter the level of cell wal and starch biosynthesis in those cells. The polynucleotides may also be used as probes for genetically and physically mapping the genes that they are a part of, and as markers for traits linked to those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nthesis
                                                                                                                    New polynucleotides encoding uridine diphosphate (UDP) glucose phosphorylase in plants and seeds, useful for creating transgenic plants which express UDP glucose phosphorylase at higher or lower levels than normal -
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                                                                                                                                                                                                                                                                                                                                                                                          Length 473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --WVAVNTAVMLIGRLPLM----NPKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                  80;
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Pred. No. 1.2;
; Mismatches 8(
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                                                                                                                                                                                      37-38; 46pp; English.
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25.3%; Pre
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   99US-0119588
                          (DUPO ) DU PONT DE NEMOURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB07948 standard; Protein;
                                                    Pearlstein RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US03513
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                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                               2000-533019/48.
                                                                                                                                                                                                                                                                                                                                              473 AA;
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                                                                                           AAA59672
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 10-FEB-1999;
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                                                  Famodu 00,
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Best Local (
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                                                                                          N-PSDB;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence; corn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 pksvievrngftfldlivigieslnkkygcsvplllmnsfnthddtgklvekysnsniei 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -SRVEA 89
                                                                                                                                     New polynucleotides encoding uridine diphosphate (UDP) glucose phosphorylase in plants and seeds, useful for creating transgenic plants which express UDP glucose phosphorylase at higher or lower levels than normal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --KGFWLPELADPIIPAI-----LKDNGYEYLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 htfnqsqyprivtedflplpskgqtgkdgwyppghgdvfpslnnsgkldtllsqgkeyvf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 iaqvpdehvnefksiekfkifntnnlwvnlkaikrlvdaealkmeiipnpkev 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 473;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --IEIIGTSYTAILPLLPL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO: 41366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.2%; Score 93; 24.9%; Pred. No.
                                                                                                                                                                                                                                     Claim 1; Page 45-46; 46pp; English.
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99US-0123180.
99US-0123548.
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(DUPO ) DU PONT DE NEMOURS
                                       Pearlstein RW;
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                                                                          WPI; 2000-533019/48.
N-PSDB; AAA59677.
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05-MAR-1999;
09-MAR-1999;
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                                   Famodu 00,
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bait polypeptide; gastric ulcer;
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                                                                                                                                                              the treatment
of recombinant
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Pred. No. 1.1;
5; Mismatches 71; Indels
                                                                                                                                                             brid system for identifying compounds useful in gastric ulcers comprises producing a collection
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                                                                                                                                                           two-hybrid system for identifying
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Search completed: April

Job time: 357 sec

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US-08-773-870-4
US-09-141-135-2
US-09-141-135-2
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US-08-156-020-2

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US-08-156-020-6

US-08-156-020-10

US-08-481-238-4

US-08-471-066B-4

US-08-471-066B-4

US-08-471-066B-4

US-08-471-066B-4

US-08-157-653-4

US-08-156-386-4

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ZIP: 92037

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/613,220B
FILING DATE: 08-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
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Pred. No. 6.8
; Mismatches
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                                                                                                                                                                                                                                                                                                             Suite
                                                                                                                                                                                                                                                          APPLICANT: Murphy, Dennis
APPLICANT: Murphy, Dennis
APPLICANT: Reid, John
TITLE OF INVENTION: ALPHA-GALACTOSII
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Sul
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                   Sequence 4, Application US/08613220B Patent No. 5958751 GENERAL INFORMATION:
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    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acid
TYPE: amino acid
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internal
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FRAGMENT TYPE:
US-08-613-220B-4
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GGIASDLIEIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPIIPA
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                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KATO, IKUNOSHIN
APPLICANT: LADERMAN, KENNETH
APPLICANT: ANFINSEN, CHRISTIAN
TITLE OF INVENTION: THE ALPHA-AMYLASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16773
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Patent No. 5366883
GENERAL INFORMATION:
APPLICANT: ASADA, KIYOZO
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NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
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UEMORI, TAKASHI
MUKAI, HIROYUKI
KATO, IKUNOSHIN
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MEDIUM TYPE: Disk
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APPLICANT:
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Length 647;

; DB 1;

Score 116.5; Pred. No. 0.

6.6%;

Similarity

Local

Query Match

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TAILPLLPLSRVEAQVQRDRVKEELFE---VSPKGFWLPE-LADPIIPAILKDNGYEYLF 131
                         EKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIEIIGTS-Y 75
     Gaps
                                                                                                                                                                                             176 RKAIKLVF-----EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKN
                                                                                                                                           -AIKPIKPLPHLIKAQREKRFRYISYLLLREL
                                                                                                  143 VDDYHFMSAGLSKEELYWPYYTEDGGEVIAVFPI------DEKLRYL--IPFRPV
                                                                                                                                                                                                                                                                        -TYEWVYEKG
                                                                                                                                                                                                                                                       230 ILLYGTDIEFIGYRDIAGRMSVEGLLEVIDELNSELCPSEL-KHSGREL-----YLRT
    131;
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
   117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KATO, IKUNOSALL.
LADERMAN, KENNETH
ANFINSEN, CHRISTIAN
INVENTION: THE ALPHA-AMYLASE GENE
  Mismatches
                                                                                                                                                                                                                                                                                                              SSWA--DKSLRIWREDEGNARLNMLYN-----MRGEL-
                                                                                                                                                                                                                                                                                                                                                                    LAENSDARGWPLPERRLDAFRAIYND--WRG 342
                                                                                                                                                                                                                                                                                                                                                                                                  -- PEARKYLLRAQCNDAYWHG 358
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RR: 95469/C-1195
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US-07-894-212A-2
; Sequence 2, Application US/07894212A
; _____ No. 5366883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9546
TELECOMMUNICATION INFORMATION:
64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASADA, KILLASADA, KILLASADA, KILLASADA, KILLAWASHI MUKAI, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 649 amino acids
Conservative
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APPLICATION NUMBER: US
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CORRESPONDENCE ADDRESS:
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                                                                                                                                        132 ADEAMLFSAHLNS---
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APPLICANT: KATO, IK
APPLICANT: LADERMAN
APPLICANT: ANFINSEN
TITLE OF INVENTION:
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79;
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Matches
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EWVYEKG
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                                                                                                                                                                   76 TAILPLLPLSRVEAQVQRDRVKEELFE---VSPKGFWLPE-LADPIIPAILKDNGYEYLF
                                                                                                                                                                                                                                                                                  RKAIKLVF------EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKN
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                                                                                                               24 EKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIE
                                                                                                                                                                                                                                                      -DEKLRYL-
                                                        Length
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                                                                        .8;
117;
                                                       DB 1;
                                                     6.6%; Score 116.5; DB.
larity 20.2%; Pred. No. 0.0018
Conservative 64; Mismatches 1.
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RR: 95470/C-1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/07893928A
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ANFINSEN, CHRISTIAN
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OPERATING SYSTEM: PC-DOC AND
SOFTWARE: PATOL
RRFF
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REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Tape
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CORRESPONDENCE ADDRESS:
protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application Patent No. 5578479 GENERAL INFORMATION:
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                                                                                                                                                                                                                             ADEAMLFSAHLNS-
                                                                  1 Similarity
79; Conserv
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; MOLECULE TYPE:
US-07-894-212A-2
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                                                         Query Match
                                                                      Best Local
Matches
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                                                                                                                                                                                                                                                                               --DEKLRYL--IPFRPV
                                                                                                                                                                                                          TAILPLLPLSRVEAQVQRDRVKEELFE --- VSPKGFWLPE - LADPIIPAILKDNGYEYLF
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                                                                                                                                                                                                                                                               --AIKPIKPLPHLIKAQREKRFRYISYLLLREL
                                                                                                                                                                                                                                                                                                                                              --TYEWVYEKG
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                                                                                                                                                   EKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIEIIGTS-Y
                                                                                                                                                                      131;
                                                                                             Length 650;
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                                                                                                                           Indels
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                                                                                              Score 116.5; DB 1;
Pred. No. 0.0019;
; Mismatches 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMBER: US/09/002,298
Filed Herewith
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TITLE OF INVENTION: HUMAN FATTY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09002298 Patent No. 6045001
                                                                                                                           64;
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Karl J.
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IBM Compatible
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                               Query Match
Best Local Similarity 20.2%;
Matches 79; Conservative
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Palo Alto
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Corley, Neil
Tang, Y. Tom
Shah, Purvi
                                           protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bandman,
Hillman,
                                                                                                                                                                                                                                                                  ADEAMLFSAHLNS - - -
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: prote
US-07-893-928A-1
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                       DB 3;
                                                                                                                                                                                                                                                  0.91;
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                                                                                                                                                                                                                                                                  Mismatches
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STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                    4.8%; Score 85.5; larity 25.0%; Pred. No. 0 Conservative 17; Mismatche
                \OmegaS
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              PF-0453
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08773870
Patent No. 5912143
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                               17;
36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Diskette
IBM Compatible
                                                                                              amino acids
                                                                  SEQUENCE CHARACTERISTICS
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acid
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                                                                                                                          single
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REGISTRATION NUMBER:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: OVARTUT02
CLONE: 2595635
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                                                                                                          amino acid
                                                                                                                                      linear
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                                                                                                                      STRANDEDNESS:
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                                                 TELEFAX: 6:
INFORMATION FOR
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                                                                                                                                      TOPOLOGY:
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                                                                                           LENGTH:
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US-08-773-870-4
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Best Local S
Matches 30
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                                                                                                      Gaps
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                                                                                                                                                                             -ASDLIEIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPIIPAIL
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|----SFVLVTSL----G
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                                                                                                                                                                                                                                                                                                                                             238 EFIGYRDIAGRMSVEGLLEVIDELNSELCPSELKHSGRELYLRTSSWADKSLRIWREDEG
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                                                                                                                        11 QYAEIPKSEPKVIEKAYIPVIE-----TLIKEEPFGLNITGYTLKFLPKDIILVKGGI
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                                                                                                     121;
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                                                                      Score 82.5; DB Pred. No. 2.6; 7; Mismatches
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20.3%; Pred. No. 16;
ive 56; Mismatches
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; Patent No. 6245969
; GENERAL INFORMATION:
; APPLICANT: Chong, Joane
; TITLE OF INVENTION: Receptor Kinase BIN1
; FILE REFERENCE: 07251/022001
; CURRENT APPLICATION NUMBER: US/08/881,706
; CURRENT FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
                                                                                                                                          85 QSAQIACSSPSVV--ASLPLDQSDEGSSSQKEE-
                                                                                                                                                                                                                                                                                                                                                               ----IWEALNAMGLYDGMEHL----
                                                                                               57;
                                                                    the similarity 19.7%; 67; Conservative
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                                                                                                                                                                                                         137 KVTDLVQFLLFKY--
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US-08-881-706-2
   GenBank
533511
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LIBRARY:
              ; CLONE:
US-08-773-870-4
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Best Local S
Matches 77
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EAQVQRDRVKEELFEVSPKGF -- - WLPELADPIIPAILKDNGYEYLFADEAMLFSAHLNS 144
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                                                                                                                                                                                                                                                                                                                                                                                      Hopkins, Sharon A
FENTION: Production of Bacillus Entomotoxins
FENTION: Methylotrophic Yeast
COUENCES: 27
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                                                                   Indels
                                       Length
                                                                                                                                                    145 AIKPIKPLPHLIKAQREKRFRYISYLLLRELRKAIKLVFEGKV 187
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3.9;
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                                      Score 82; DB Pred. No. 2.5; 77; Mismatches
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; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33,129
3R: 52627
                                                                                                                                                                                                                                                    23, Application US/08231342
). 5827684
                                                                                                                                                                                                                                                                                               Sreekrishna, Kotikar
Prevatt, William D
Thill, Gregory P
Davis, Geneva R
Koutz, Patricia
Barr, Kathryn A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-372-7842
TELEFAX: 312-372-7848
                                                                  17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23:
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                                      4.6%;
illarity 29.1%;
Conservative 1
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 amino acids
amino acid
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ADDRESSEE: Fitch, Even,
STREET: 135 S. LaSalle
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60603-4277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312-37
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                       Patent No. 5827684
GENERAL INFORMATION:
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chicago
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-08-231-342-23
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STREET: 13
CITY: Chic
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APPLICANT:
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US-09-286-805-4
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Best Local $
                                          Query Match
Best Local
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             279
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; Patent No. 6117990
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth E.
; TITLE OF INVENTION: DNA Encoding Orphan SNORF1 Receptor
; FILE REFERENCE: 58987
; CURRENT APPLICATION NUMBER: US/09/286,805
; CURRENT FILING DATE: 1999-04-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0 - beta
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                                                                        -MRGELAFLAENSDARGW-
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Pred. No. 1.4;
77; Mismatches
                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 1942/31
CURRENT APPLICATION NUMBER: US/09/141,135
CURRENT FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: WordPerfect 6.1/Windows
                 IEFIGYRDIAGRMSVEGLLEVIDELNSELCPSEL
                                                                        RTSSWADKSLRIWREDEGNARLNMLYN-
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US-09-141-135-2
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ilarity 20.1%;
Conservative 3
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LENGTH: 338
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81 LLPLSRVEAQVQRDRVK-EELFEVSPKGFWLPELADPIIPA
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                          ASWIEDKNILLYGTDIEFIGYRDIAGRMSVEGLL-
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Pred. No.
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22-JAN-1997
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FR: GM50002
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5. 5989864
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APPLICATION NUMBER: 60/029329
FILING DATE: 29-OCT-1996
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01-NOV-1996
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Burnham, Marc..
Gentry, Daniel
Hodgson, John
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
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IBM Compatible
SYSTEM: DOS
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FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskett
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                            APPLICANT: Lawlor,
TITLE OF INVENTION:
                                                                                                                                359 RYVKYALAREF---
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APPLICANT: Burnha
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MOLECULE TYPE:
-08-788-892-2
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APPLICANT:
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                                                                                                                                                                                                                                                                Patent No.
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Similarity 63; Conserv

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                -GIASDLIEIIGTSYT--AILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWL
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                                                                                                                                                                   LLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRL-----PLMNPKKVASWI
                                                                                                                                                                                       58 EIRTSKHSYGPSRDWLKIVKSSSAKGKIKSFFKKQDRSSNIEKGRMMVEV-EIKEQGF--
                                                                                                                                                                                                                                --GLLEVIDELNS
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 -IETLIKEEPFGLNITGYTLKFLPKDIILVKG--
                                                                                                                            5' TO 3' EXONUCLEASE MUTATIONS OF THERMOSTABLE DNA POLYMERASES
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US/07/977,434
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Patent No. 5466591;
GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
Abramson, Richard D.
TTCANT: Abramson, Richard D.
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28-SEP-1990
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FILING DATE: 28-SEP-1990
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PRIOR APPLICATION DATA:
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15-MAY-1990
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22-AUG-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 Kingsland Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07
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MEDIUM TYPE: Floppy
COMPUTER: Macintosh
OPERATING SYSTEM: 7
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
FILING DATE: 28-SEP-
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IOR APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                     8753
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                                                                                                                                                                                                                                                                                    5466591
                                      APPLICATION NUMBER: WO PCT/US90/07641 FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                     Case No.
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                                                                                                                                                               FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NATA
                                                                              APPLICATION NUMBER: US 585,471 FILING DATE: 20-SEP-1990 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 455,611 FILING DATE: 22-DEC-1989
                                                                                                                                                                                                              APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
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Patent No. 5795762
746,121
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, Richard D.
5' TO 3' EX
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NUMBER: US 7
15-AUG-1991
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amino acid
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                           PRIOR APPLICATION DATA:
                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                          NAME: Luann Cserr
REGISTRATION NUMBER:
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APPLICANT: Gelfand, I
APPLICANT: Abramson,
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85; Conser
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US-07-977-434-4
            FILING DATE:
APPLICATION
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THERMOSTABLE DNA POLYMERASES 38
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                                                                                                                                                                                                                                                  02-JUN-1995
N: 435
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APPLICATION NUMBER: 07/97,434
FILING DATE: 23-FEB-1993
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,213
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143,441
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION MINITED
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FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
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20-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 746,121 FILING DATE: 15-AUG-1991 PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 31,822
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                                                                                                                                                                                                                                       WordPerfect 2.1
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
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amino acid
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APPLICATION NUMBER: US
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      TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                         New Jersey
07110-1199
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US-08-458-819-4
                                                                                                  CITY: Nutley STATE: New Ju
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STRIEVLEELAGEHEIIPLILEY--RKIQKLKSTYIDALPKMVNPKTG--RIHASFNQTG
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                             142;
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     Length 893;
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Reichert, Fred L.
/ENTION: MUTANT CHIMERIC DNA POLYMERASE
                            103;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
   1;
     DB
                           Mismatches
  Score 82; DB
Pred. No. 11;
                                                                                                                                                                               430 FLGYKMTSYQELMSFSFPLFGFSFADVPV---
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Branchburg
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                                                                                                                                                                                                                                    ---SLKLHEADLENVFYKI
                                                                                                                                                                                                                                                              -YGTDIEFIG---YRDIAG-
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Patent No. 6228628
GENERAL INFORMATION:
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                         49;
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NAME: Petry Ph.D., Douglas A
REGISTRATION NUMBER: 35321
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 4.68; 22.48;
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(510)814-2977
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amino acid
                           Conservative
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COUNTRY: United States
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MEDIUM TYPE: Floppy
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FILING DATE:
CLASSIFICATION:
            Similarity
85; Conser
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TOPOLOGY: lin
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US-09-105-697-10
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APPLICANT:
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Query Match
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STATE:
          Best Loc
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                                  Gaps
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                                                           --VIETL--IKEEPFGLNITGYTLKFLPKDIILVKGGI
                                                                                                                  ASDLIEIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPIIPAILK
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                                                                                                                                                                                                                                                                                                                                                       ---LEVIDEL--NSELCPSELKHSGRELYLRTSSWADKSLRIWREDEGNARLNMLYNMRG
                                                                                                                                                                                                                                  LRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKNILL-
                                                                                                                                        Length 893;
                                                                                                                                                                         124 DNGYEYLFADEAMLFSAHL---NSAIKPIKPLPHLIKAQREKRFRY----
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PCT-US91-07035-4

Sequence 4, Application PC/TUS9107035

GENERAL INFORMATION:
APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
                                                                                                                                                                                                                                                                                                  --RMSVEGL--
                               103;
 Score 82; DB 4;
Pred. No. 11;
); Mismatches 10
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                                                                                                                                                                                                                                                                                              --YGTDIEFIG---YRDIAG--
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: 1400 Fifty-third Street
Emeryville
California
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28-SEP-1990
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28-SEP-1990
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                             49;
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4.68; 22.48;
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                                                                                                                                                                                                                                                                                                                                                                                                               310 ELAFLAENSDARGWPLPER 328
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           Similarity 22.45; Conservative
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
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OPERATING SYSTEM:
                                                        EPKVIEKAYIP--
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CITY: Emer
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PRIOR APPLICATION DATA:
APPLICATION NATA:
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Pred. No.
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
                         MBER: US 063,509
17-JUN-1987
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                 MBER: US 746,121
15-AUG-1991
                                                                                                                                                                                                           JMBER: US 585,471
20-SEP-1990
                                                                         IMBER: US 899,241
22-AUG-1986
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--VEPVPPYFDT--
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ER: 32,630
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TELEPHONE: 415-420-3300
INFORMATION FOR SEQ ID NO: 4:
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nilarity 22.4%;
Conservative 4
FILING DATE: 12-JAN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06
FILING DATE: 17-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sias Ph.D, Stacey REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 893 amino acids
TYPE: AMINO ACID
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                                                                        APPLICATION NUMBER: FILING DATE: 22-AUG-PRIOR APPLICATION DATA:
                                                                                                                                   FILING DATE: 15-AUG-
NOR APPLICATION DATA:
APPLICATION NUMBER:
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Matches 85; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ropology: 1; Molecule Type: PCT-US91-07035-4
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4, 2002, 14:40:44 Search completed: April Job time: 193 sec

4.5 Compugen Ltd version - 2000 GenCore (c) 1993 Copyright

model ΜS using protein search, OM protein Search time 21.67 Seconds (without alignments) 1216.262 Million cell updates/sec •-2002, 14:38:16 4, April Run on:

US-09-407-806A-4 1778 1 LRALVFHGNLQYAEIPKSEP.....ERRLDAFRAIYNDWRGNGEP Perfect score: Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

76174552 residues 219241 seqs, Searched:

219241 hits satisfying chosen parameters Total number of

length: 0 length: 2000000000 length: sed Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_68:\* Database

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. score gand is Pred.

#### SUMMARIES

Description	hypothetical prot	lase A (EC 3.	bable a	lpha-amylase (	-amylase (E	n heav	oullulanas	ial assembl	-amyl	inum	dehydrogenas	ulan	netical prot	ted	thetical prot	chetical	thetical	thetical p	polymeras	rected RNA	probable ferredoxi	etical	direct	5 protein homo	se II	tical 138.	obable DNA r	served hypothe	probable serine/th
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### ALIGNMENT

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Dispected process horikoshil C; Species: Pyrococcus horikoshil C; Species: Pyrococcus horikoshil C; Species: Pyrococcus horikoshil C; Species: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 08-Sep-2000 C; Accession: E71144

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu DNA Res. 5, 55-76, 1998

A; Title: Complete sequence and gene organization of the genome of a hyper-thermophil. A; Reference number: A71000; MUID:98344137

A; Recession: E71144

A; Ratus: preliminary; nucleic acid sequence not shown; translation not shown A; Residues: 1-364 <KAW>
A; Residues: 1-364 <KAW>
A; Residues: 1-364 <KAW>
A; Residues: train OT3
A; Experimental source: strain OT3
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBanatal Source: Strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBanatal Source: Strain OT3

A;Note: this accession replaces an increme contics:
A;Genetics:
A;Gene: PH0368
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0368

18; 18; Length 364; Indels ch 1 Similarity 72.2%; Pred. No. 4.5e-86; 262; Conservative 47; Mismatches 36; Query Match Best Local S Matches 262

229 240 180 114 171 DPIIPAILKDNGYEYLFAD-EAMLFSAHLNSAIKPIKPL-PHLIKAQREKRFRYISYLL-121 172 181 115 QΩ δ Db Qγ pp δ g Qγ

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6.8%; Score 120.5; Dillarity 20.1%; Pred. No. 0.22; Conservative 62; Mismatches
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J.; Kushida,
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-IPFADPEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELFEV
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YTYMQRVKPKGR-IYLPTASYREMMEWVLFPEAQKELEELVEKLKTENLWDKFSPYVKGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156;
                                                                                                                                                                                               a)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----DKDKVQQIKKLNKYIY
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                                                                                                                                                                                                                                                                                  PID
                                                                       ALURAN

amylase A (EC 3.2.1.-) - Dictyoglomus thermophilum
C; Species: Dictyoglomus thermophilum
C; Species: Dictyoglomus thermophilum
C; Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change
C; Accession: S00628; A34969
R; Fukusumi, S.; Kamizono, A.; Horinouchi, S.; Beppu, T.
Eur. J. Biochem. 174, 15-21, 1988
A; Title: Cloning and nucleotide sequence of a heat-stable amylas
A; Reference number: S00628; MUID:88225097
A; Accession: S00628
A; Molecule type: DNA
A; Residues: 1-686 <FUK>
A; Accession: A34969
A; Molecule type: protein
A; Residues: 2-13 <FUK2>
C; Genetics:
A; Residues: 2-13 <FUK2>
C; Genetics:
A; Residues: amyA
C; Superfamily: Dictyoglomus thermophilum amylase A
C; Keywords: glycosidase; hydrolase
F; 2-686/Product: amylase A #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 686;
                                                                                                                        #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Pyrococcus horikoshii
C; Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
C; Accession: G71241
R; Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.; Horikawa, H.; Haikawa, Y.; Hino,
T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---IILVKGGIASDLIEIIGTSYTAILPLLPLSRVEAQVQRDRVKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --EDKN--ILLYGTDIEFIGYRDIAGRMSVEGLLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.5%; Score 151; DB 1;
21.6%; Pred. No. 0.0011;
ive 63; Mismatches 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----ADKSLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable alpha-amylase - Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 KLKIMAERGQIEF----VSGGFYEPILPIIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 ELCPSELKHSGRELYLRTSSW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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361 NGK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 IWRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASWI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
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DNA Res. 5, 55-76, 1998
A; Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A; Reference number: A71000; MUID: 98344137
A; Accession: G71241
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-633 < KAW>
A; Residues: 1-633 < KAW>
A; Residues: 1-632 < KAW>
A; Residues: 1-632 < KAW>
A; Residues: 1-632 < KAW>
A; Residues: 1-633 < KAW>
A; Cross-references: GB: APO00001; NID: 93236128; PIDN: BAA29262.1; PID: 93256579
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBa A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: Dictyoglomus thermophilum amylase A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Pyrococcus abyssi (strain Ors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PID:9545
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C; Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Accession: E75206
R; anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A; Reference number: A75001
A; Accession: E75206
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 TSYTAILPLLP-LSRVEAQVQRDRVKEELFEVSPKGFWLPE-LADPIIPAILKDNGYEYL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --AIKPIKPLPHLIKAQREKRFRYISYLLLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 KVIEKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIE-IIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | || :| :| : | : | || || || || || GEYEPILVAIPEEDRVE-QIKLSKGWARKMGYEARGLWLTERVWEPELVKTLREAGIEYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DEKLRYL--IPFRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDELNSELCPSELKHSGRELYLRTSSWADKSLRIWREDEGN---ARLNMLYNMRGELAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --WLKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --LEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDRISSDDKINLMLYS -- - EYLSKFRPKGLVYLPIASYFEMSEWSLPARQAKLFFEFIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 LRKAIKLVF-----EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EDK-NILLYGTDIEFIG-----YRDIAG--RMSVEGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 VNETLEYLHSLADEDESKVAVFHDDGEKFGAWPGTHELVYERG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 126.5; DI
Pred. No. 0.075,
59; Mismatches
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C;Superfamily: Dictyoglomus thermophilum amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 ILDDYHFMSAGLSKEELFWPYYTENGGEAIVVFPI---
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A; Residues: 1-655 <KAW>
A; Cross-references: GB:AJ248283; GB:AL096836;
A; Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PTARIFVLRAQCNDAYWHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
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20;

Gaps

135;

Indels

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Oy Db	24 EKAYIPVIETLIKEEPFGLNITGYTLKFLPKDIILVKGGIASDLIEIIGTS-Y 75         : :    :::    :::	230 ILLYGTDIEFIGY
Qy Db	76 TAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPE-LADPIIPAILKDNG 126 	Qy 282 SSWADKSLRIWREDEG
Oy Db	127 YEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYISYL 170   :  :     :     :     :        :	314
δλ	171 LLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASW 224   :     :     :         186 PFRPVDKVISYLHSLASEDESKVAVFHDDGEKFGIWPMTYEW 227	5 33/ LVRNNESULT 6
oy Oy	IEDKGRM : :  VYEKGWLREFFDRVSSDEAINIMLYSEYLQKFKPKGLVYLPIASYFEMSEWSLPAQQAKL	heavy chain, cytosol tains: dynein ATPase ( cies: Dictyostelium di
QQ Dp	250 SVEGLLEVIDELNSELCPSELKHSGRELYLRTSSWADKSLRIWREDEGNARLNMLYNMRG 309    :  :     :  :     309 	Date: 03-Feb-1994 #seque; Accession: A44357; S2850; Koonce, M.P.; Grissom, P. Cell Biol. 119, 1597-16
Qy	310 ELAFLAENSDARGWPLPERRLDAFRAIYNDWRG 342   :     :       :    337LRDNPSARRFVLRAQCNDAYWHG 359	A44 A44 Sid
RESC A4999 a1ph C;SF	ase Py No	
A A A A A A A A A A A A A A A A A A A	erman, K.A.; erman, K.A.; ol. Chem. 268 le: alpha-Amy erence number ession: A4951	F;2669-2676/Region: nucleoti F;3011-3018/Region: nucleoti F;1975/Binding site: ATP (L) F;2277/Binding site: ATP (L) F;2675/Binding site: ATP (L) F;3017/Binding site: ATP (L)
	ecule type: Didues: 1-649 ss-references etics:	Query Match Best Local Similarity 2 Matches 80; Conservati
ល្យជាចំល	tart codon: GTG unction: escription: catalyzes the hydrolysis of internal 1,4-alph athway: glycogen/starch degradation uperfamily: Dictyoglomus thermophilum amylase A	3358
ž Ž	words: glycosidase; hydrolase; polysaccharide degradation	QY /2 GTSYTAILPLEPLSKVEJ :  : :  ::  Db 3398 -LAMEAVCLMLGGKKLEV
ŌĔĬ	Query Match Best Local Similarity 20.2%; Pred. No. 0.45; Matches 79; Conservative 64; Mismatches 117; Indels 131; Gaps 21;	Qy 127 YEYLFADEAMLFSAHLN:   ::    3457 FDYETVN
QY	24 EKAYIPVIETLIKEEPFGLNITGYTLKFLPKDIILVKGGIASDLIEIIGTS-Y 75 	185 GKVTLKVKDIEA
Qy	76 TAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPE-LADPIIPAILKDNGYEYLF 131 	245
Qy	132 ADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYISYLLLREL 175  :	305
Qy	176 RKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKN 229   :: :         :   :     1   :     1   :	331 DAFRAIYNDWRGNGEP

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BL:215124; NID:97226; PIDN:CAA78827.1; PID:97227
cted from NCBI backbone (NCBIP:121195)
heavy chain, cytosolic
otetramer; hydrolase; microtubule binding; nucleotide binding motif A (P-loop)
cleotide-binding motif A (P-loop)
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281
                                                     276
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                                                                                                                                                    - -AF
   -YLRT
                                                                                                                                                                                                                                                                                                                                                                                                                        olic - slime mold (Dictyostelium discoideum) (EC 3.6.1.33) discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --EAVSTIKKKH---LD----EIKSLPKPPTPVK-
   AGRMSVEGLLEVIDELNSELCPSEL-KHSGREL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122;
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                                                                                                                DEGNARLNMLYN-----MRGEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 111; DE 21.3%; Pred. No. 19; tive 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ENSDARGWPL-
                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                               342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P.M.; McIntosh, J.R
604, 1992
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                                                                                                                                                                                                                                 RLDAFRAIYND--WRG
                                                                                                                                                                                                                                                                   quence not shown
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|NLNSE
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346

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A; Wolecule type: DNA
A; Residues: 1-392 <SIM>
A; Cross-references: GB:AE003888; GB:AE003849; NID:g9105187; PIDN:AAF83179.1; GSPDB:GN
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carraro submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Franco, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, R.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, A.M.; Verlyovski-Almeida, S.; Vettore, A.L. A; Contence number: A59328
A; Contetics: annotation
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-amylase (EC 3.2.1.1) - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Date: 13-Sep-1996 #sequence_revision 12-Sep-1996 #text_change 21-Jul-2000
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
FReich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
From, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Schautors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A;Reference number: A64300; MUID:96337999
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Mesidues: 1-467 kBUL>
A;Residues: C;Genetics:
A;Map position: FOR1586396-1587799
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----KGFWLPELADPIIPAILKDNGYEYLFADEAML 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIPVIETLIKEEPF-GLNITGYTLKFLPKDIILVKGGIASDLIEIIGTSYTAILPLLPLS 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R----SGNRFKVEHYAVEPLPLNAVAERGIVEVEQVGEAIRRAVSRSGTKAKFAAAAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LLQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             221 VASWIEDKNILLYGTDIEFIGYRDIAGRMSVEGLLEVIDELNSELCPSELKHSGRELYLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 FSAHLNSAIKPIKPLP----HLIKAQRE-KRFRYISY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.0%; Score 106.5; I Similarity 24.2%; Pred. No. 1.3; 0; Conservative 34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 EQLFGGKQL----TDEVMHRYGMTYEEAGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVEAQVQRDRVKEELFEVSP---
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Best Local S
Matches 80
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C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C; Accession: A75207
R; anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome strud.
A; Reference number: A75001
A; Reference number: A75001
A; Reference number: A75007
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1362 < KAW>
A; Residues: 1-1362 < KAW>
A; Residues: 1-1362 < KAW>
C; Genetics: Strain Orsay
C; Genetics: C; Genet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135
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|-FRAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---SRVEAQVQR--DRVKEEL--FEVSPKGFWLPE--LADPIIPAILKDNGYEYLFADEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 VLEKLGVPKTIESYYKPWVAQFGDKKIYLFPRNHDLSDRVGFRYAGMNQYDAVKNFVEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IETLIKEEPFGLNITGYTLKFLPKDIILVKGGIASDLIEIIGTSYTAILPLLPL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 LKIQKQNYDGSL-VYVITLDGENPW----EHYPFDGKLFLEELYRQLEELQKKGLIRTVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1362
                                                                                                                                                                                                            C;Ŝpecies: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               459 PSEYIEMFGDKANKLTPKMMKRLDFTTEDNVNALLKAKTLGELYDMVGVTE---
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                                                                                                                                                                                    · Pyrococcus abyssi (strain Orsay)
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 110;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2%; Scilarity 21.9%; Pr
Conservative 61;
        -NWHANSLP
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Best Local Simi
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Best Local Similarity
Local Similarity
es 89; Conser
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tatus predicted <HEA>
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                                                                                                                                                                                                                 42 KVANKCYIPTNELILELIDEYDFKVNYSITGVFVEQALEFNDYVLDLFKDLVKTGNVELI 101
                                                                                                                                    Gaps
                                                                                                                                                                     21 KVIEKAYIP---VIETLIKEEPFGLN--ITG----YTLKFLPKDIILVKGGIASDLIEII 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:940408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLNKFDE
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                                                                                                                                                                                                                                                                                                  102 AETYHH -- SLTSLFETEDEFIEDIEMHRKMYKEIFGFKAKVFRNTELIYNNRIAKIAKDL
                                                                                                                                                                                                                                                                                                                                          GYEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYIS----YLLLRELRKAIKL
                                                                                                                                                                                                                                                                                                                                                                     --EKILGWRSPNYLYQSPDGMKILLRNYRLSDDI
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                                                                                                                                105;
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A; Residues: 1-27, 'E', 29-1251 <POU>
A; Cross-references: EMBL:X62088; NID:940379
A; Cross-references: EMBL:X62088; NID:940379
A; Experimental source: strains ATCC 43181 and ATCC 43755
B; Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; J. Gen. Microbiol. 137, 519-525, 1991
A; Title: Cloning of a DNA fragment encoding the 5'-terminus of A; Reference number: S16145; MUID:91237316
A; Reference number: S16145; MUID:91237316
A; Residues: 1-229, 'M', 231-252 <FUJ>
A; Residues: 1-229, 'M', 231-252 <FUJ>
A; Residues: 1-229, 'M', 231-252 <FUJ>
C; Comment: The clostridial neurotoxins are toxins that inhibit C; Comment: The heavy chain mediates the binding of toxin to cell C; Superfamily: tetanus toxin
C; Comment: The heavy chain mediates the binding of toxin to cell C; Superfamily: tetanus toxin
C; Comment: Dotulinum neurotoxin type E light chain #statu F; 2-422/Product: botulinum neurotoxin type E heavy chain #statu F; 412-426/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    botulinum neurotoxin type E precursor - Clostridium butyricum
C;Species: Clostridium butyricum
C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keywords: neurotoxin
2-422/Product: botulinum neurotoxin type E light chain #statu
423-1251/Product: botulinum neurotoxin type E heavy chain #st
412-426/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 FATISWADTERDVSAWL---GNKMQRISFEKLKDIGKFIKENSNKL----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: EMBL:X53180; NID:g40407; PIDN:CAA37321.1; Experimental source: strain BL6340
Comment: The clostridial neurotoxins are toxins that inhibit
Comment: The heavy chain mediates the binding of toxin to cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LTADKYAIWLASTPGEVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Pathway: glycogen/starch degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                          Length
                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            VFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 FGEHHWKETGIFEFLRYLPIEIAKHEHLEVVNVSEVVDRLEPR-
                                                                                                                                  130;
                                                                                           DB 2;
                                                                                        th 6.0%; Score 106.5; I Similarity 23.0%; Pred. No. 1.6; 84; Conservative 47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: nucleic acid sequence not shown
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,'E',29-1251
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A; Accession: JH0256
A; Status: nucleic aci
A; Molecule type: DNA
A; Residues: 1-27,'E',
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                                                                                                Query Match
                                                                                                                     Local
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RESULT 11
S52737
NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
N;Alternate names: mitochondrial complex I 76K chain
C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Date: 19-May-1995 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C;Accession: S52737
R;Rasmusson, A.G.; Grohmann, L.
Submitted to the EMBL Data Library, March 1995
A;Accession: S52737
A;Accession: S52737
A;Accession: S52737
A;Accession: S52737
A;Accession: S52737
A;Accession: S52737
A;Coss-references: EMBL:X85808; NID:9758339; PIDN:CAA59818.1; PID:9758340
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 11
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 11
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --HLNSAIKP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245
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                    Gaps
                                                                     --PKDIILVKGGIA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 CYHSRLSIAGNCRMCLVEVEKSPKPVASCAMPALPGMKIKTDTPIAKKAREGVMEFLLMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LDCPIC-----DQGGECDLQDQSMAFGSDRGRFTEMKRSVVDKNLGPLVKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208 V -- MTRCIQCTRCVRFASEVAGVEDLGMLGRGSGEEIGTYVEKLMTSELSGNVIDICPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- LPLMNPKKVASWIEDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGRMSVEGLLEVIDELNSELCPSELKHSGRELYLRTSSWADKSL-----RIWREDEGNA
                                                                                                                    523 LDAQKVPEGENNV---NLTSSIDTALLEQP--KIYTFFSSEFINNVNKPVQAALFVGWIQ
                                                                                                                                                                                                          -AIKLVFEGK---VTLKVK-----DIEAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                IVSNWMTKINTQFNKRKEQMYQALQNQVNALKAIIESKYNSYTLEEKNELTNKYDIEQIE
                                                                                                                                                                                                                                                                            -PELADPIIPAILKDNGYEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYISY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PVWVAVN----TAVMLIGRLPLMNPKKVASWIE-DKNILLYGTDIEFIGYRDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TSYTAILPLLPLS-RVEAQVQRDRVKEELFEVSPKGFWL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 140;
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                      111;
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                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 RLNMLY-----NMRGELAFLAENSDARGWPLPERRLDAFRAIYND
                                                                        LQYAEIPKSEPKVIEKAYIPVIETLIKEEPFGLNITGYTLKFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133;
                      139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 AEIPKSEPKVIEKAYIPVIETLIKEEPFGLNITGYTLKFLPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 102; DB 2;
llarity 20.8%; Pred. No. 6.8;
Conservative 58; Mismatches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 SPKGFWLPELADPIIPAILKDNGYEYLFADEAMLFSA----
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d. No. 9.1; Mismatches
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                       67;
                          Conservative
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qa	266 ALTSKPFAFKARNWELKGTESIDVTDAVGSNIRIDSRGPEVMRVVPRLNEDINEEWISDK 325	C;Species:
Oy	NILLYGTDIEFIGYRDIAGRMSVEGLLEVIDELNSELCPSEL	C; Date: 20-A C; Accession:
QΩ	ALAIVAEVMH	R;Bevan, M.; ewes, H.W.;
δ <sub>γ</sub>	271KHSGRELYLRTSSWADKSLRIWREDEGNARLNMLYNMRGELAFLAENSDA 320	submitted to A; Reference
Q T	3//	A, Accession: A, Status: pr A, Molecule t
RES T08	SULT 12 8162	A;Residues: A;Cross-refe
amy C:S	lopullulanase (EC 3.2.1) - Pyrococcus furiosus	A; Experiment C; Genetics:
C C; D	ate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999 ccession: T08162	
R;D App	, C.; Zeikus, J.G. obiol. 63, 3577-3584	T1E
A A A	ssion 21	Query Matc
ξ <b>Α</b> Α	cession: r08162 tatus: preliminary; translated from GB/EMBL/DDBJ	Matches
A 4	JON>	Qy 1 LR
) (j (j	LOSS-references: EMBL:AF016588; NID:g2435436; PIDN:AAB71229.1; PID:g2435438 enetics:	Db 143 LT
5 € Q ₹		Oy 56 III
Ω, χ. Σ, χ.	sscription: hydrolyzes alpha-1,6 and alpha-1,4 linkages in starch-related polysacchar sywords: glycosidase; hydrolase; polysaccharide degradation	Db 200 VLI
ć		Qy 105 PKC
ō й S	cc	Db 259 RRI
Ĕ	90; Conservative 60; Mismatche	Qy 163 RFF
ò i		   DD 308 FFF
ga -		Oy 217 N
δò	GYTLKFLPKDIILVKGGIAS	: Db 361 HLQ
qq	228 GYTREDLKTVLYHQMWLLNNTFKEHEKINLLLGNGNVEVTVVPYAHPIGPILN 280	OY 257 VID
ΟY	85SRVEAQVQRDRVKEELFEVSPKGFWLPELADPIIPAILKDNGYEYL 130	;  Db 406 MIR
QQ	281 DFGWSEDFDAHVKKAHELYKKYLGGGVATPRGGWAAESALNDKTL-EILAENGWQWV 336	315
δδ	131 FADEAML 170	454
QQ	QYEAV	, ,
Qy	171LLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDK 228	RESULT 14
Dp		DNA-directed
ΟY	229 NILLYGTDIEFIG-YRDIAGRMSVEGLLEVIDELNSELCPS-ELKHSGRELY 278	0
QQ	OLAGVTEE	R; Read, T.D.;
Οy	AENSDARGWPI. DERRITDARBA	Nucleic Acids
qq		A;Title: Genc A;Reference n
QY		A; Status: pre
qa		A;Molecule ty A;Residues: 1
		A; Cross-refere A; Experimenta]

hypothetical protein T1E3.40 - Arabidopsis thaliana

RESULT T48464

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ome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 number: A81500; MUID: 20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA polymerase, beta' chain TC0588 [imported] - Chlamydia muridarum (str
hlamydia muridarum, Chlamydia trachomatis MoPn
far-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000
F81686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lype: DNA
1-1396 <TET>
erences: GB:AE002328; GB:AE002160; NID:g7190627; PIDN:AAF39420.1; PID:g719
tal source: strain Nigg (MoPn)
Arabidopsis thaliana (mouse-ear cress)

Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

1: T48464

1: Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, Rudd, S.; Lemcke, K.; Mayer, K.F.X.

1: Rudd, S.; Lemcke, R.; Mayer, R.F.X.

2: the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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TVVAVSGNMEIAEALVAKNPKLLEIPGINGQIPVV---VAVENTQMEMARYLYTRTPVQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'RYIS-----YLLLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLM 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|| : | |
----FNLLYGLDDRKYLLLA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RALVFHGNLQYAE-IPKSEPKVIE----KAYIPVIETLIKEEPFGLNITGYTLKFLPKD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLAEDGYHGTLLFLNAIFYRMLGKGFLGIQATHIFGGFDLYLFFFIQLD-IALDLFNMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGFWLPELADPIIPAILKDNGYEYLFADEAMLFSAHLNSAIK-PIKPLP-HLIKAQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLAVTKHLQIESIPII-----VLASKPDLFP---GIQVKLPTLPKPSHANKDHKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELNSELCPSELKHSGRELYLRTSSWADKSLRIWREDEGNARLNMLYNM--RGELAFL
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A;Gene: TC0588
C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---YGTDIEFIGYRDIAGRMSVEGLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                        erences: EMBL:AL162972
tal source: cultivar Columbia; BAC clone T1E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.7%; Score 101.5; I
21.2%; Pred. No. 6.9;
Live 59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RN-NSELLWSTRTSSSSTLFLLAVEFRQEKV----
                                                                                                                                                                                                                                                                                                                                                                             286/1; 350/1; 493/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| | :| | :|
DSDGNGVLHLAGFPSPPSKL 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSDAR-----GWPLPERRL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -PKKVASWIEDKNILL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                         type: DNA: 1-705 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
81; Conserva
                                                                                                                                                                                                   reliminary
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59/1; 2
33.40
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hypothetical protein PAB1309 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: F75006
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: F75006
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-394 <KAWW>
A;Residues: 1-394 <KAWW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:g5458060; PIDN:CAB50492.1; PID:g545906
C;Genetics:
A;Gene: PAB1309
                                18;
                                                                                                                                                                                                                                                                                                                                    670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 LIEIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPIIPAILKDNG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --VGLAVKGKIRELVGVFREG- 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYISYLLLRELRKAIKLVFEGK 186
                                                                                                                                                                                                                                                                                                                                                                                     -TGGWASG 104
                                                                                                                                                                                  170
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                                                                                                                                                                                                                567
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                                                                                                                                                                                                                                             -MLIGRLPLMN 217
                                                                                | : |:| : |:| : : ::
404 IQRGAPEVWD-----VLEEIIKGHPVLLNRAPTLHRLGIQAFEPVLIEGK-AIRVHPLVC 457
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                                Gaps
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                                                                                                                                                                                  -QREKRFRYISYL
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                                                                                                                                                                                                      -LKDAYDK
                                                                                                                                         84;
                             :68
  1396;
                                                                                                                         TSYTA-----ILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPI-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 39
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                                                               IPKSEPKVIEKAYIPVIETLIKEEPFGLN--ITGYTLKFLPKDIILVKGGIA
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   Length
                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :99
Score 101.5; DB 2;
Pred. No. 18;
2; Mismatches 142;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB Pred. No. 3.3;
                                                                                                                                                                                                                                              LLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAV-
                                                                                                                                                                                  GYEYLFADEAMLFSAHLNSAIKPIKPLPHLIKA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
Ouery Match
Best Local Similarity 22.3%; Pr
Matches 84; Conservative 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 320 ARGWPLPERRLDAFRAI 336
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DVIILG-AYSALLPYVP--
                                                                                                                                                                                                                                                                                                                                                                      LYLRTSSWAD----
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Qy 246 AGRMSV 251
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Db 229 LGVLSI 234
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Search completed: April 4, 2002, 14:41:20 Job time: 184 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

4, 2002, 14:40:46; Search time 12.46 Seconds (without alignments) 1018.140 Million cell updates/sec April Run on:

....ERRLDAFRAIYNDWRGNGEP 346 US-09-407-806A-4 1778 1 LRALVFHGNLQYAEIPKSEP..... Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched: 100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result		a)				
NO.	Scor	Match	Length	DB	OI	Description
7	151	ω	99		MY1_DI	9660
7	26.	7.1	633		AMYA_PYRHO	57932 pyrococcu
m	•		S		AMYA_PYRAB	v298 pyrococcu
4	16.	_	Ť		AMYA_PYRFU	067 pyrococ
ហ	11	_	7		DYHC_DICDI	1036 di
9	06.		9		AMYA_METJA	3006 methanoc
7	•		S		BXE_CLOBU	995 clostridi
80	10	-	738		NUAM_SOLTU	8644 solanum
σ	01.		σ		RPOC_CHLMU	ok79 chlamyd
10	0		ıO		MALO_PYRKO	2450
11	99		$\sim$		YZ35_METJA	1291
12	7		S		MALQ_THELI	2462 thermoco
13	7		$\circ$		RPOC_CHLTR	1316
14	9	•	$\sim$		DPOL_BPSP1	314 bacter
15	96.5		36		DPO3_THEMA	shi6 thermotog
16	o	5.4	_		1	3346 escher
17	96	5.4	24		MSH6_YEAST	3834 saccharomy
18	95.5	5.4	_			64459 pyrus pyri
.19	o	•	9			9sdx3
20	93		~			3772 hordeum
21	93		Φ,		DP3X_MYCPN	75177
22	92		1		ILVI_BUCAI	57321
23	91		S		Y288_THEMA	9wyc4 thermo
24	90.5		$\mathbf{\omega}$		YG5B_YEAST	53316 sacchar
25	O	•	-		PPOX_BACSU	32397 bacil
26	9	•	w		HEMZ_SYNY3	54225 syne
27	6		446		SR54_BACSU	105 bacillus
28		-	1-			46818 sinapis
29	œ	•	4		SR54_MYCMY	01442 mycopla
30	88	•	m,		VBR1_TMOV	06661 tomato m
31	88	•	1-		PT1_STAAU	1183 staphyloc
32	w	4.9	592	٦	В3_Н	0186 homo sapi
33	87.5	•			UDPG_SOLTU	עכ

Q58611 methanococc P50546 arabidopsis	P41258 campylobact P95928 sulfolobus	Q92999 chlamydia p	Posses rnizosium s P46207 aquifex pyr		P32073 dictyosteli	хутетта		P35169 saccnaromyc
YC14_METJA RPOB_ARATH	SYK_CAMJE	RPOC_CHLPN	Y4TK_RHISN	GTAZ_MOUSE	GUAA_DICDI	SYFB_XYLFA	DP3A_THEAQ	TOR1_YEAST
<del></del>				٦,	æ	<b>,</b>	1	Н
1018	501	1393	331	221	718	792	1220	2470
4.9 9.4	4 v	4.9			•	•	•	•
87.5	86,5	86.5	98	85.5	5	85.5	85	82
3.4 5.5	36	38	39	4 7	42	43	44	45

## ALIGNMENTS

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collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
          103
                                                                      162
                                      IYDKFGQ 115
                                                                                                     156
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                                                                                                                                                                  ADPEET 194
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Oguchi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagai Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
         ELFEV
                                                                                                      ¥
                                                                                                                        RFRYISYLLLRELRKAIKL-VFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thermophilic archaebacterium, Pyrococcus horikoshii OT3.";

DNA Res. 5:55-76(1998).

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

-!- PATHWAY: POLYSACCHARIDE DEGRADATION.

-!- SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y. Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohf Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi Masuchi Y., Shizuya H., Kikuchi H.; "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
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                                                                                                                                                                                                                                                                     SPKGFWLPE-LADPIIPAILKDNGYEYLFADEAMLFSAHLNSAIKPIKPLPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase: Glycosidase; Carbohydrate metabolism; Complete pr
SEQUENCE 633 AA; 75017 MW; 9DCBCBB2FE191501 CRC64;
                                     -DKDKVQQIKKLNKY
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ng as its content
---IILVKGGIASDLIEIIGTSYTAILPLLPLSRVEAQVQRDRVKE-
                                                                                                                                                                                      --EDKN--ILLYGTDIEFIGYRDIAGRMSVEGLLE--
                                                                               --ADKSLR---
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39, Last sequence update)
40, Last annotation update)
3.2.1.1).
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                   68 KLKIMAERGQIEF----VSGGFYEPILPIIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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20-AUG-2001 (Rel. 4
ALPHA-AMYLASE (EC 3
AMYA OR PH0193.
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30-MAY-2000
30-MAY-2000
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                                                                                                                                                                                                                                  174
                                                                                                                                                                                                                                                                                                                                           237
                                           Gaps
                                                                    KVIEKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIE-IIG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                           TSYTAILPLLP-LSRVEAQVQRDRVKEELFEVSPKGFWLPE-LADPIIPAILKDNGYEYL
                                                                                          --AIKPIKPLPHLIKAQREKRFRYISYLLLRE
                                                                                                                                                                                                                                                                  ----DEKLRYL--IPFRP
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                                                                                                                                                                                                                                                                                                                                                                                                    238 FDRISSDDKINLMLYS---EYLSKFRPKGLVYLPIASYFEMSEWSLPARQAKLFFEFIKK
                                                                                                                                                                                                                                                                                           LRKAIKLVF-----EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWI---
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CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
PATHWAY: POLYSACCHARIDE DEGRADATION.
SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LFEKYRIFVRGGIWKN---FLYKYPEGNYMHKRMLMLSKL-
                                           Indels
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                                                                                                                                                                                                                                                                                                                             190 VNETLEYLHSLADEDESKVAVFHDDGEKFGAWPGTHELVYERG-
Score 126.5; DB 1;
Pred. No. 0.026;
; Mismatches 121;
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Hydrolase; Glycosidase; Carbohydrate metabolism;
SEQUENCE 655 AA; 77296 MW; 7F6F920B1A00EECE (
                                                                                                                                                                                                                                                         143 ILDDYHFMSAGLSKEELFWPYYTENGGEAIVVFPI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 AENSDARGWPLPERRLDAFRAIYND--WRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PTARIFVLRAQCNDAYWHG
                                     59;
 Similarity 22.3%; 7; Conservative
                                                                                                                                                                                                                     131 FADEAMLFSAHLNS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Pyrococcus abyssi
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                               87;
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Query Match
Best Local :
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                                Matches
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Gaps

135;

Indels

117;

Length 655;

DB 1;

Score 120.5; Di Pred. No. 0.079 2; Mismatches

6.8%; ilarity 20.1%; Conservative 63

Similarity

Query Match Local

79;

Matches

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                        170
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                                                                   126
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                                                                                                   --KEDRLEQIYLLKEWAKKIGYDAKGLWLTERVWQPELVKTLREAG
                                                                                                                                                                                                           -EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASW
                                                                                                                                      ----AIKPIKPLPHLIKAQREKRFRYISYL
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                                                                                                                                                                         --DEKLRYL--I
                                                                     -ELFEVSPKGFWLPE-LADPIIPAILKDNG
--PKDIILVKGGIASDLIEI1GTS-Y
                   28 EKAYRPFLE-ILEEYPNMKVAIHISGILVEWLEENKPDYIDLLKSLVRKGQVEIVVAGFY
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SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: DISPLAYS A BROAD RANGE OF SUBSTRATE SPECIFIED CAPACITY TO HYDROLYZE CARBOHYDRATES AS SIMPLE AS CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCCLINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.

PATHWAY: POLYSACCHARIDE DEGRADATION.
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                                                                                                                                                                                                                                              -- PM-
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Privalov P.L., Anfinsen C.B.;
"The purification and characterization of an extremely tlalpha-amylase from the hyperthermophilic archaebacterium furiosus":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
NCBI_TaxID=2261;
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Anfinsen C.B.;
                                                                                                                                                                                                                                                                                  -NILLYGTDIE-----FIGYRDIA
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Last sequence update)
Last annotation update)
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 EKAYIPVIETLIKEEP---FGLNITGYTLKFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -WHG
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MEDLINE=94043280; PubMed=8226990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 ----LRDNPSARRFVLRAQCNDAY-
                                                                       TAILPLLPLSRVEAQVQRDRVKE
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                                                                                                                                           YEYLFADEAMLFSAHLNS-
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01-FEB-1996 (Rel. 33,
20-AUG-2001 (Rel. 40,
ALPHA-AMYLASE (EC 3.2.
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                                                                                                                                                                                                                171 LLRELRKAIKLVF-
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DEKLRYL--IPFRPV 190
                                                                                                                                                                                                                                                                                                24 EKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIEIIGTS-Y 75
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                                                                                                                                                                                                                                                                                                                                                                                                      87 EPVLASIP---KEDRIEQIRLMKEWAKSIGFDARGVWLTERVWOPELVKTLKESGIDYVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TYEWVYEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                        -AIKPIKPLPHLIKAQREKRFRYISYLLLREL
                                                                                                                                                                                                                                                                                                                                28 EKCYWPFLETL-EEYPNMKVAIHTSGPLIEWLQDNRPEYIDLLRSLVKRGQVEIVVAGFY
                                                                                                                                                                                                                            Length 648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95170719; PubMed=7866389;
Koonce M.P., Grissom P.M., Lyon M., Pope T., McIntosh J.R.;
"Molecular characterization of a cytoplasmic dynein from
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 ILLYGTDIEFIGYRDIAGRMSVEGLLEVIDELNSELCPSEL-KHSGREL--
                                                                                                                                                                            BF7A495F084E0FB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium.
                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                  117;
                                                                                                                       EMBL; L22346; AAA72035.1; -.
Hydrolase; Glycosidase; Carbohydrate metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSWA--DKSLRIWREDEGNARLNMLYN-----MRGEL--
                                                                                                                                                                                                                                6.6%; Score 116.5; Di
20.2%; Pred. No. 0.16;
ive 64; Mismatches
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J. Eukaryot. Microbiol. 41:645-651(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyosteliida; NCBI_TaxID=44689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=AX3;
MEDLINE=93107159; PubMed=1469051;
                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                76178 MW;
                                                                                                                                                                                                                                                     Local Similarity 20.2 nes 79; Conservative
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                                                                                                                                                                                648 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYHC_DICDI
P34036;
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                                                                                                                                                                                    SEQUENCE
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 FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS MOTOR FOR THE INTRACELLULAR RETROGRADE MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES.
SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF
                                                                                                                               in
                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMI the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-score or send an email to license@isb-sib.ch).
                                           INTERMEDIATE AND LIGHT CHAINS.
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY
                                                                                                                                                                                                                          Coiled
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9A0319915D579D3A CRC64
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COIL (POTENTIAL)
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1969
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S28504; S
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DOMAIN 86
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17; 3397 3456 --KSIATYKEEYATLIRET--EQIKTES 3545 **EQLEN 3501** GTSYTAILPLLPLSRVEAQVQRDRVKEELFEVS-----PKGFWLPELADPIIPAILKDNG 126 YEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYISYLL--LRELRKAIKLVFE 184 244 304 PERRL 330 Gaps YAEIPKSEPKVIEKAYIPVIETLIKEEPFGLNITGYTLKFLPKDIILVKGGIASDLIEII LEDPG GKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKNILLYGTDIEFIGYRD IAGRMSVEGLLEVIDELNSELCPSELKHSGRELYLRTSSWADKSLRIWREDEGNARLNML PEERL -WEQOSENFNTOM-126; STVVGDVVLASAFLAYIGFFDQNFRTDLMRKWMIRLDSVGIKFKSDLSVPSFLSKP --ETVNRASKACGPLVKWATAO----TYYSEILDRIKPLREEV Length 4725; Indels YADLEKAEPAIIEAQ--EAVSTIKKKH---LD----EIKSLPKPPTPVK 122; DB 1; 6.2%; Score 111; DE larity 21.3%; Pred. No. 6.3; Conservative 48; Mismatches -ENSDARGWPL SKVKNKVDRSIALLDNLNSE--AANELKLKODEIVATITALE-DAFRAIYNDWRGNGEP -NWHANSLP --AFLA-Similarity YNMRGEL-80; Query Match Best Local 3457 FDY 3358 12 Matches 185 245 302 3581 331 ŏ g δλ ŏ Q δ d Dp ŏ

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                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; Hydrolase; Glycosidase; Carbohydrate metabolism;
Complete proteome.
SEQUENCE 467 AA; 55558 MW; 40A6B1CDDD4D967E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 GTSYTAILPLIPLSRVEAQVQRD ----RVKEELFEVSPKGFWLPELA-DPIIPAILKDN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 KVANKCYIPTNELILELIDEYDFKVNYSITGVFVEQALEFNDYVLDLFKDLVKTGNVELI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 GYEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREKRFRYIS----YLLLRELRKAIKL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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                      AMYA_METJA STANDARD; PRT; 467 AA. 059006; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PUTATIVE ALPHA-AMYLASE (EC 3.2.1.1).
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Mismatches
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Conservative 47;
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                                                                                                                                                                                                                               Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                  Methanococcus
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Best Local (
AMYA_METJA
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SPINAL CORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: DISULFIDE-LINKED HETERODIMER OF A LIGHT CHAIN (L) AND A HEAVY CHAIN (H). THE LIGHT CHAIN HAS THE PHARMACOLOGICAL ACTIVITY, WHILE THE N-AND C-TERMINAL OF THE HEAVY CHAIN MEDIATE CHANNEL FORMATION AND TOXIN BINDING, RESPECTIVELY.

SUBCELLULAR LOCATION: SECRETED.

MISCELLANEOUS: THERE ARE SEVEN ANTIGENICALLY DISTINCT FORMS OF BOTULINUM NEUROTOXIN: TYPES A, B, C1, D, E, F, AND G.

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                  (strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEURONS.
                                                                                                                                                                                                                                                                                                                                                                           Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.; "Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strain ATCC 43181 and ATCC 43755)."; Biochem. Biophys. Res. Commun. 183:107-113(1992).
                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
NCBI_TaxID=1492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMITTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                icum;
                                                                                                                                                                                                            (BONT/E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the BL6340.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gimenez J., Foley J., Dasgupta B.R.;
"Neurotoxin type E from Clostridium botulinum and C. butyripartial sequence and comparison.";
FASEB J. 2:A1750-A1750(1988).
-1- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANS RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restiuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by ancentities requires a license agreement (See http://www.isb-gorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                           (69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-251 FROM N.A.
STRAIN=BL6340;
MEDLINE=91237316; PubMed=2033376;
Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki Yokosawa N., Yashiki T., Oguma K.;
"Cloning of a DNA fragment encoding the 5'-terminus type E toxin gene from Clostridium butyricum strain J., Gen. Microbiol. 137:519-525(1991).
                                                                                                                                                                                                         . 24
                                                                                                                                                    01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
BOTULINUM NEUROTOXIN TYPE E PRECURSOR (EC 3.4
                                                                                                                                                                                                                                                                                                                                              , AND ATCC 43755;
PubMed=1543481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62088; CAA43998.1;
EMBL; X53180; CAA37321.1;
PIR; JH0256; JH0256.
PIR; S16145; S16145.
                                                                                                                     STANDARD;
                                                                                                                                                                                                                                        butyricum.
                                                                                                                                                                                                                                                                                                                          FROM N.A.
TCC 43181,
                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC 43181,
MEDLINE=92181428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENDOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF 1-48.
                                                                                                                                                                                                                        (BONTOXILYSIN E)
Clostridium buty
                                342 IYKMYK 347
                                                                                                                                                   01-JUL-1993
01-JUL-1993
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF STRAIN=5262;
IYNDWR
                                                                                                                   BXE_CLOBU P30995;
                                                                                                                                                                                                                                                                                                                             SEQUENCE
336
                                                                                                   BXE_CLOBU
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                                                                                                                                                                                                                                                                                                                   --PKDIILVKGGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVSNWMTKINTQFNKRKEQMYQALQNQVNALKAIIESKYNSYTLEEKNELTNKYDIEQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SSYTDDKILISYFNKFFKRIKSSS
                                                                                                                                                                                                                                                                                                                                -DIEAV-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --RIWREDEGNA
                                                                                                                                                                                                                                                                                                                                                                    -TSYTAILPLLPLS-RVEAQVQRDRVKEELFEVSPKGFWL--
                                                                                                                                                                                                                                                                                                                                                                                              QVLVDFTTEANQKSTVDKIADISIVVPYIGLALNIGNEAQKGNFKDAL-ELLGAGILLEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracheophyta
                                                                                                                               E, LIGHT-CHAIN
E, HEAVY-CHAIN
                                                                                                                                                                                                                                                               Length 1250;
                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                   SIMILARITY)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo|
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                     Transmembrane; Hydrolase; Metalloprotease; Zinc.
                                                                                                                                           BOTULINUM NEUROTOXIN E, HEAVY ZINC (CATALYTIC) (BY SIMILARI BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARI INTERCHAIN (PROBABLE).
K -> M (IN REF. 2).
MW; 8171B5B2C2312857 CRC64;
                                                                                                                                                                                                                                                                                         Indels
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STRAIN=CV. DESIREE; TISSUE=Leaf;
Rasmusson A.G., Grohmann L.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            892
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 75 KDA SUBUNIT, MITOCHO (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-75KD) (CI-75KD)
MITOCHONDRIAL COMPLEX I SUBUNIT).
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|---GIYND
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                                                                                                                               BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                       139;
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                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                   Score 104.5; Di
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        MEROPS; M27.002; -.
InterPro; IPR000395; Bontoxilysin.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
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ММ
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 P04958;
                                                                                                  Neurotoxin; I
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Q43644;
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                                  SIMILARITY).

CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

COFACTOR: MAY BIND ONE 2FE-2S CLUSTER & ONE 4FE-4S CLUSTER.

SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS (BY SIMILARITY).

SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

SIMILARITY: BELONGS TO THE COMPLEX I 75 KDA SUBUNIT FAMILY.

SIMILARITY: BELONGS TO THE COMPLEX I 75 KDA SUBUNIT FAMILY.
     AND IT IS A
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                               IS OXIDIZED
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(POTENTIAL)
(POTENTIAL)
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OXIDOREDUCTASE
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FUNCTION: THIS IS THE LARGEST SUBUNIT OF COMPLEX I COMPONENT OF THE IRON-SULFUR (IP) FRAGMENT OF THE FORM PART OF THE ACTIVE SITE CREVICE WHERE NADH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion;
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IRON-SULFUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT
                                                                                                                                                                                                                                                                                                                      Molybdopterin
                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00641; COMPLEX1_75K_1; PROSITE; PS00642; COMPLEX1_75K_2; PROSITE; PS00643; COMPLEX1_75K_3; Oxidoreductase; NAD; Ubiquinone; M
                                                                                                                                                                                                                                                                                      Complex1_75
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.PF00384; molybdopterin;
                                                                                                                                                                                                                                                                           EMBL; X85808; CAA59818.1;
InterPro; IPR000283; Compl
InterPro; IPR001041; Ferre
InterPro; IPR001467; Molyk
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738
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TRANSIT
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                                                                                                -AQVQRDRVKEELFEV 103
                                                                                                                    CYHSRLSIAGNCRMCLVEVEKSPKPVASCAMPALPGMKIKTDTPIAKKAREGVMEFLLMN 159
                                                                                                                                                                      207
                          Gaps
                                                  56
                                                              : : || :| :||
-VFVDGYPVK-IPKGMTVLQACEIAGVDIPRF
                                                                                                                                                                   -DQGGECDLQDQSMAFGSDRGRFTEMKRSVVDKNLGPLVKT
                                                                                                                                                                                             VFEG
                                                                                                                                                                                                                    ICPVG
                                                                                                                                               -HLNSAIKP
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                                                                                                                                                                                                                                           -LPLMNPKKVASWIEDK
                         140;
                                                                                                                                                                                                                 V--MTRCIOCTRCVRFASEVAGVEDLGMLGRGSGEEIGTYVEKLMTSELSGNVIDJ
                                                                                                                                                                                            -RYISYLLLRELR-KAIKI
  Length 738;
                          Indels
                                              AEIPKSEPKVIEKAYIPVIETLIKEEPFGLNITGYTLKFLPK
  DB 1;
                                                                                             --ILVKGGIASDLIEIIGTS---YTAILPLLPLSRVE-
                                                                                                                                                                                                                                           -VKDIEAVPVWVAVNTAVMLIGR---
                                                                                                                                            SPKGFWLPELADPIIPAILKDNGYEYLFADEAMLFSA-
             ed. No. 2.5 Mismatches
Score 102;
             Pred.
                        58;
                                                                     SDLPKRHPVGGARVHLPNPEDVIE-
Similarity 20.8%; 37; Conservative
                                                                                                                                                                    -LDCPIC-
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                    87;
Query Match
           Local
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                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salzberg S.L.,
 -GTDIEF--IGYRDIAGRMSVEGLLEVIDELNSELCPSEL-- 270
                                          -ALAIVAEVMHQIKPEEIVG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404 IQRGAPEVWD-----VLEEIIKGHPVLLNRAPTLHRLGIQAFEPVLIEGK-AIRVHPLVC 457
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                                                                                     -- NARLNMLYNMRGELAFLAENSDA 320
                                                                                                             HAIN (EC 2.7.7.6) (TRANSCRIPTASE SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGMA CHAIN AND THE CORE CHAINS, 1 BETA CHAIN, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.F.,
K., Bass 9
Dodson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPI-IPAILKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=MOPn / Nigg;

MEDLINE=20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Balinher K., Weidman J., Khouri H., Craven B., Bowman C., Dodsor Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzbe Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Transferase; DNA-directed RNA polymerase; Transcription; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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                                                                                                                                                                                                                                 RPOC_CHLMU STANDARD; PRT; 1396 AA. 09PK79; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2 BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.7%; Score 101.5; I larity 22.3%; Pred. No. 6.6; Conservative 62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: THE ENZYME CONSISTS OF THE ENZYME WHICH IS COMPOSED OF 2 ALPHA
                                                                                     ---KHSGRELYLRTSSWADK--SLRIWREDEG-
                                          TRFFYDGLKRQRLNDPMIRGADGRFQAVSWRD-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ro; IPR000722; RNA_pol_A.
PF00623; RNA_pol A: 1
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TIGR; TC0588; -.
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229 NILLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and expression of the 4-alpha-glucanotransferase the hyperthermophilic archaeon Pyrococcus sp. KOD1, and characterization of the enzyme.";
J. Ferment. Bioeng. 83:540-548(1997).
A NEW 4-POSITION IN AN ACCEPTOR, WHICH MAY BE GLUCOSE ALPHA-D-GLUCAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb or send an email to license@isb-sib.ch).
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Transferase; Glycosyltransferase; Carbohydrate metabolism
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g as its content
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NCBI_TaxID=69014;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) (AMYLOMALTASE)
(DISPROPORTIONATING ENZYME) (D-ENZYME).
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larity 19.3%; Pred. No. 2.8;
Conservative 67; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                       228
-DEKLRYL--IPFRPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GIASDLIEIIG
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                                                                                                                    --LEVID
                                                                                                                                                                                               ELNSELCPSELKHSGRELYLRTSSWADKSLRIWREDEGNARLNMLYNMRGELAFLAENSD
                                                                                                                                                                                                                                    -VRNNPE
                                       -EGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDK--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcaceae;
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Il protein; Complete proteome.
630 AA; 72441 MW; FD8EAE30D2F5B58E CRC64;
                                                                                                                                                                                                                                    --KENKFDRYRVFVRGGIWKNFFFKYPESNYMHKRMLMVSKA-
                                                                                                                   --FIGYRDIAG--RMSVEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 EPKV-IEKAYIPVIETLIKEEPFGLNITGYTLKFLPKDIILVKG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.6%; Score 99.5; Di 20.6%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales;
  DDYHFMSAGLSKDELFWPYYTEDGGEVITVFPI
                                                                           KTLEYLHSLDDGDESKVAVFHDDGEKFGVWPG-
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InterPro; IPR002936; Toprim.
                                                                                                                     -NILLYGTDIE---
                                                                                                                                                                                                                                                                                                                   -WHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L77118; AAC37104.1;
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                                                                                                                                                                                                                                                                                                343 AREFILRAQCNDAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
Les 72; Conser
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Hypothetical
SEQUENCE 63
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                                         KAIKLVF
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20-AUG-2001
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Q60291;
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STRAIN=DSM 5473;

MEDLINE=97454300; PubMed=9310375;

Jeon B.-S., Taguchi H., Sakai H., Ohshima T., Wakagi T., Matsuzawa H.;

"4-alpha-glucanotransferase from the hyperthermophilic archaeon
Thermococcus litoralis. Enzyme purification and characterization, and gene cloning, sequencing and expression in Escherichia coli.";

Eur. J. Biochem. 248:171-178(1997).

-!- FUNCTION: CATALYZES THE TRANSGLYCOSYLATION OF

MALTOOLIGOSACCHARIDES, YIELDING MALTOOLIGOSACCHARIDES OF VARIOUS
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus
NCBI_TaxID=2265;
                                                                                                     -FSYIIIPYAQRSLKEM 458
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                       -GY-FLF
   YEYLF
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                                                                                                                                                                                                                                          KIFGA
                                                                                                                                                                          -KNVKIAKDMGL
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                                                                                                                                                                                                                            SEGMENT OF A 1,4-ALPHA-D WHICH MAY BE GLUCOSE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a
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TSY-TAILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPIIPAILKDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: INHIBITED BY P-CHLOROMERCURIBENZOIC A MONOIODOACETIC ACID, MERCURY AND NICKEL IONS.
MISCELLANEOUS: OPTIMAL ACTIVITY IS FOUND AT 90 DEGREES C SIMILARITY: BELONGS TO FAMILY 57 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                            336
                                                                                                                                     IKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKNI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carbohydrate metabolism.
                                                                                                                                                                                                                                                                           -GWPLPERRLDAFRAI
                                                                                                                                                                                                                                                                                                           -DSGRSI
                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25) (AMYLOMALTASE)
(DISPROPORTIONATING ENZYME) (D-ENZYME).
                                                                   -FSAHLNSAIKPIKPLPHLIKAQREKRFRYISYLLL
                                  -DTG--AVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                               659 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE
                               373 EGYPTELL ---- ATRIFYPFRGSRLSESLAR-
                                                                                                                                                                                                                                                                           WREDEGNARLNMLYNMRGELAFLAENSDAR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTHS AND GLUCOSE.
CATALYTIC ACTIVITY: TRANSFERS A SANEW 4-POSITION IN AN ACCEPTOR,
                                                                                                                                                                        --FLIADNDEEGL
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Ferase; Glycosyltransferase;
TE 352 352 PROB.
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032462;
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73
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Gaps

103;

Indels

134;

Length 659;

DB 1;

th 5.5%; Score 97.5; DI Similarity 18.6%; Pred. No. 4.9; 70; Conservative 69; Mismatches

Query Match Best Local

Best Loc Matches

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mydia trachomatis.";
nce 282:754-759(1998).
FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                               270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (EC 2.7.7.6) (TRANSCRIPTASE
BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT).
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KAYIPVIETL -- IKEEPFGLNITGYTLKFL ----PKDIILVKGGIASDLIEIIGTS-YTA
                                     RSYRPFMEILEEFPEMKVNVHFSGPLLEWIEENKPDYLDLLRSLIKRGQLEIVVAGFYEP
                                                                                                                 89 VLAAIP--KEDRLVQIEMLKDYARKLGYDAKGVWLTERVWQPELVKSLREAGIEYVVVDD
                                                                                                                                                                                                                                                                                                                - EL
                                                                                                                                                                                                                                                                      --TYEWVYEKGWLR
                                                                                                                                                                                                                                                                                                                                                                                           KHSGR----ELYLRTSSWADKSLRIWREDEGNARLNMLYNMRGELAFLAENSDARGWPLP
                                                                            ILPLLPLSRVEAQVQRDRVKEELFEV - - SPKGFWLPE - LADPIIPAILKDNGYEYLFADE
                                                                                                                                                         -AIKPIKPLPHLIKAQREKRFRYISYLLLRELRKA
                                                                                                                                                                                         --DEKLRYL--IPFRPVKKT
                                                                                                                                                                                                                                   -GKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKNILL
                                                                                                                                                                                                                                                                                                                                                                                                                   EFFDAITSNEKINLMTYSEYLSKFTPRGLVYLPIASYFEMSEWSLPAKQAKLFVEFVEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., A.
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V
                                                                                                                                                                                                                                                                                                               --IEFIGYRDIAGRMSVEGLLEV----IDELNSELCPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNA(N).
SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS,
                                                                                                                                                                                                                                                                        194 IEYLESLTSDDPSKVAVFHDDGEKFGVWPG--
                                                                                                                                                                                             147 YHFMSAGLSKEELFWPYYTEDGGEVITVFPI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE001304; AAC67907.1; -. Pro; IPR000722; RNA_pol_A. PF00623; RNA_pol_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERRLDAFRAIYNDWRG
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OR CT314.
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                                                                                                                                                                                                                                                                                                               YGTD--
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Pfam; PF0
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of
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MEDLINE=91004249; PubMed=2119891;
Goodrich-Blair H., Scarlato V., Gott J.M., Xu M.Q., Shub D "A self-splicing group I intron in the DNA polymerase gene Bacillus subtilis bacteriophage SPO1.";
Cell 63:417-424(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shub D.A.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA
EXHIBITS A 3' TO 5'. EXONUCLEASE ACTIVITY.
-!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
N PYROPHOSPHATE + DNA(N).
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                                                                                                                                                                                -ILPLLPLSRVEAQVQRDRVKEELFEVSPKGFWLPELADPI-
                                                                                                                                                    404 IQRGAPEVWD-----VLEEIIKGHPVLLNRAPTLHRLGIQAFEPVLIEGK-A
     Transcription;
                                                                                                 Indels
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                             B24BF8841D284065 CRC64
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                                                                    Score 97.5; DB
Pred. No. 13;
62; Mismatches
                                                                                                                                                                                                                                                                                           LLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
Transferase; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                    GYEYLFADEAMLFSAHLNSAIKPIKPLPHLIKA--
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01-FEB-1994 (Rel. 28, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
DNA POLYMERASE (EC 2.7.7.7).
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"The DNA polymerase-encoding gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92380475; PubMed=1324872;
                            154904 MW;
                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage SP01.
Viruses; dsDNA viruses, no RNA
SP01-like Viruses.
                                                                    sh. Similarity 22.0%; 83; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      730 ARGNKSQLKQLGALRGL 746
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                            1396 AA;
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            Complete proteome SEQUENCE 1396 A
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P30314;
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                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00447; DNA_POLYMERASE_A; 1.
Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
Exonuclease; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKFLPKDIILVKGGIASDLIEIIGTSYTAILPLLPLSRVEAQVQRDRVKEELFEVSPKGF 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --TKVRGKLYEIEGRKF
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 SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                   OF821B13B5A05EE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                092HF6;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA POLYMERASE III POLC-TYPE (EC 2.7.7.7) (POLIII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 97;
Pred. No. 8
                                                                                                                                                           EMBL; M84415; AAA03732.1; ALT_SEQ.
EMBL; M37686; AAA64535.1; -.
PIR; JC1269; JC1269.
HSSP; P00582; IKRP.
InterPro; IPR002562; 3_5_exonuclease.
InterPro; IPR001098; DNA_poll.
InterPro; IPR001098; DNA_poll.
Pfam; PF01612; 3_5_exonuclease; 1.
Pfam; PF00476; DNA_pol_A.
PRINTS; PR00868; DNAPOLI.
SMART; SM00474; 35EXOC; 1.
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Thermotoga maritima.
Bacteria; Thermotogales; Thermotoga.
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MEDLINE=99045593; PubMed=9826752;
Huang Y.P., Ito J.;
                                                                                                                                                                                                                                                                                                                                                                                                           106837 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th 5.5%; Sc
Similarity 18.1%; Pr
65; Conservative 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                 924 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SAHLNSAIKP--IKPLPHLIKAQREKRFRYISYLLLRELRKAIKLVFEGKVTLKVKDIE 195
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                                                                                                                                                                             STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria fr
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
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"The hyperthermophilic bacterium Thermotoga maritima has two diclasses of family C DNA polymerases: evolutionary implications Nucleic Acids Res. 26:5300-5309(1998).
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TYPE-C FAMILY. POLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: REQUIRED FOR REPLICATIVE DNA SYNTHESIS. THIS POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N). SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY). SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. PC
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EMBL; AE001732; AAD35661.1;
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RTSSWADKSLRIWREDEGNARLNMLYNMRGELAFLAENSDARG-----WPLPERRLDAFR 334
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539 DYTALKPFHCTILVQNKKGLKNLYKLVSDSYIKYFYGVPRILKSELIENREGLLVGSAC-
                                                           ---ISGELGRAALEGASDSELEEIAKFYDYIEVMPLDVIAEDEEDLDRERLKEVYRKLY-
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                                   239 FIGYRDIAGRMSVEGL-
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4, 2002, 14:40:16 ; Search time 28.84 Seconds (without alignments) 1754.862 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-407-806A-4 1778 1 LRALVFHGNLQYAEIPKSEP.....ERRLDAFRAIYNDWRGNGEP 346 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\*
sp\_invertebrate:\*
sp\_mammal:\*
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sp\_organelle:\*
sp\_phage:\*
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1: sp\_archea:\*
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7: sp\_mhc:\*
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11: sp\_rodent:\*
12: sp\_virus:\*
13: sp\_virus:\*
14: sp\_unclass

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

KIES	Description	O9hhb5 pyrococcus		_		30	Q9far6 clostridium	030772 pyrococcus	$\overline{}$	Q9uyc0 pyrococcus		Q9pkb1 chlamydia m		Q58793 methanococc	Q9avf4 amaranthus	017474 hydra oliga	Q9iar8 salmo salar	xyle]		032462 thermococcu
SUMMAKIES	ID	 09HHB5	058106	Q9V294	Q9PGD3	Q9MBD0	Q9FAR6	030772	Q9LZ29	Q9UYC0	032450	Q9PKB1	058818	058793	Q9AVF4	017474	Q9IAR8	Q9PA87	0899WX0	032462
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# ALIGNMENTS

SEQUENCE FROM N.A. STRAIN=DSM 3638; Verhees C.H.; Submitted (OCT-199 EMBL; AF195244; AA; SEQUENCE 364 AA; Ouery Match Best Local Similarity Matches 273; Conser 1 LRALVFHGNLQYA :
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230 -ILLYGTDIEFIGYRDIAG-RMSVEGLLEVIDELNSEL-CPSELKHSGRELYLRTSSWA- 285

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WEDLINE=98344137; PubMed=9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nag
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku
A Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogu
A Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
A Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
T. Complete sequence and gene organization of the genome of a hyp
T hermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
EMBL; AP0000002; BAA29442.1; -.
R Hypothetical protein; Complete proteome.
SEQUENCE 364 AA; 41755 MW; 7B4B36AB4A975BAD CRC64;
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                                                                                                                                                                                                                                    Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
NCBI_TaxID=53953;
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                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 41.8 KDA PROTEIN PH0368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.1%; Score 1229; DB 1; 72.2%; Pred. No. 1.2e-78; ive 47; Mismatches 36
                                                                                                                                                          364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 Similarity 72.2
262; Conservative
                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
                                                                                          ||:
NGK 363
                                                                              345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGE 345
                                                                              NGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                        058106
058106;
                                                                                                                                                                                                                           PH0368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Loc
Matches
                                                                              343
                                                                                                   361
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                                                                                                                                    RESULT
058106
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"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248283; CAB49104.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                       Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SRVEAQVQR--DRVKEEL--FEVSPKGFWLPE--LADPIIPAILKDNGYEYLFADEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 PSEYIEMFGDKANKLTPKMMKRLDFTTEDNVNALLKAKTLGELYDMVGVTE-----EMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LLLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 LRTSSWADKSLRIW-REDEGNARLNMLYNMRGELAFLAENSD-ARGWPLPERRLDAFRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --IETLIKEEPFGLNITGYTLKFLPKDIILVKGGIASDLIEIIGTSYTAILPLLPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 RKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKNILLYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 LKIQKQNYDGSL-VYVITLDGENPW----EHYPFDGKLFLEELYRQLEELQKKGLIRTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 VLEKLGVPKTIESYYKPWVAQFGDKKIYLFPRNHDLSDRVGFRYAGMNQYDAVKNFVEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --SVEGLL--EVIDELNSELCPSELKHSGRELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1362;
                                                                                                                                                                                                                                                                                                                                                                                                 277AFAB4E14860D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KPIKPLPHLIKAQREKRFRYISY--
                                                                           (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09PGD3;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FIMBRIAL ASSEMBLY MEMBRANE PROTEIN.
XF0369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150;
                                         1362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 110; DB 21.9%; Pred. No. 40; ive 61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QYAEIPKSEPKV-----IEKAYIPV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                              154578 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 DIEFIG-YRDIAGRM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
SEQUENCE 1362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                       Pyrococcus abyssi.
                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=ORSAY; Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLFSAHLNSAI - -
                                                                                                          01-MAR-2001 (TrEMI
AMYLOPULLULANASE.
                                                                                                                                                    APU OR PAB0122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 YNDW 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        568 GSDW 571
                                                       Q9V294;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93;
                                       09V294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9PGD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174
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RESULT
09V294
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16;
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                                                                                                                                    Simpson A.J., Fulnweel=1091034;

A Simpson A.J., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
A Alvarenga R., Alvaelach F.C., Arruda J.E., Baia G.S., Baptista C.S.,
A Alvarenga R., Alvaelach E.D., Bordin S., Bove J.M., Briones M.R.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
A Barros M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
A Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
A Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
A Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
A Lemos E.G.M., Lemos M.V., Martins E.N., Marchado J.A.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Marsukuma A.Y.,
A Marques M.V., Martins E.A.L., Martins E.M.F., Marsukuma A.Y.,
A Marques M.V., Marcins E.A.L., Martins E.M.F., Marsukuma A.Y.,
A Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
A Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
A Quaggio R.B., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
A da Silva A.C., Jerenti M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira J.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
A da Silveira M.F., Truffi D., Tsai M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 YIPVIETLIKEEPF-GLNITGYTLKFLPKDIILVKGGIASDLIEIIGTSYTAILPLLPLS 85
                                                                                                                                                                                                                                     Neto C.M.,
                                                                                                                                                                                                                                                                                                                             Jima J.P.,
Jima J.P.,
L.C.C.,
No J.A.,
                                                                                                                                                                                                                                                             Dorry H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASWIEDKNILLYGTDIEFIGYRDIAGRMSVEGLLEVIDELNSELCPSELKHSGRELYLR
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                                                                                                                                                   Abreu F.A., Acencio M.,
Saia G.S., Baptista C.S.,
Bove J.M., Briones M.R.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LLOLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSAVITKLI-----PMPVGLDEQDLEAQIEIEATNYIPYPIEEVSLDFEVLGPVPNNTEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LLLR------ELRK-AIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- LAVENAFSLIAQELSVGSNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lva A.M., da Silva F.R., Silva W.A. Jr., estri M.L.Z., Siqueira W.J., de Souza A.A., M.F., Truffi D., Tsai S.M., Tsuhako M.H., M.A., Verjovski-Almeida S., Vettore A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lanis J., Setubal J.C.;
the plant pathogen Xylella fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119;
 :dno.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92;
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KGFWLPELADPIIPAILKDNGYEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC45F485326D28BD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --HLIKAQRE-KRFRYISY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 106.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 11;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVLLAASRSENVELRQSALEL---GGLTAKVIDVEA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DIGATMSTLNVL
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                                                                                                                                 MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Souza A.P., Terenzı m.t., de Souza A.P., Terenzı m.A., Verje Vallada H., Van Sluys M.A., Verje "... Meidanis J.,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42118 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001023; HSP70. PRINTS; PR00301; HEATSHOCK70 Complete proteome. SEQUENCE 392 AA: 42118 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome sequence of the e 406:151-159(2000). AE003888; AAF83179.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVEAQVQRDRVKEELFEVSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                        FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQLFGGKQL-
                                             NCBI_TaxID=2371;
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                                                                                                             STRAIN=9A5C
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                                                                                         SEQUENCE
                             Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
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RESULT Q9MBD0

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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UDP-GLUCOSE PYROPHOSPHORYLASE.
Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Rosaceae; Pyrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 VVPHAGLEPA--PKDTAEI--KALLDKLVVLKLNGGLGTTMGCTG-----PKSVIEVRD 104
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CV. NIJISSEIKI;
Norioka S., Kiyozumi D., Norioka N.;
Norioka S., Kiyozumi D., Norioka N.;
Molecular cloning and nucleotide sequencing of a gene encoding UDP-glucose pyrophosphorylase of Japanese pear (Pyrus pyrifolia Nakai).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB027617; BAA96250.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LVFHGNLQYAEIPKSEPKVIEKAYIPVIETLIKEEPFG--LNITGYTLKFLPKDIILVKG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsukamoto K., Gyobu Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=BL 6340/ATCC 43755/BL 5520/KZ 147;
STRAIN=BL 6340/ATCC 43755/BL 5520/KZ 147;
MEDLINE=20509829; PubMed=11055954;
Wang X., Maegawa T., Karasawa T., Kozaki S., Tsukamoto K., Gyobu Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
Yamakawa K., Oguma K., Sakaguchi Y., Nakamura S.;
"Genetic Analysis of Type E Botulinum Toxin-Producing Clostridium butyricum Strains.";
Appl. Environ. Microbiol. 66:4992-4997(2000).
EMBL; AB039264; BAB12249.1; -.
InterPro; IPR000395; Bontoxilysin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 458;
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Last annotation update)
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458 AA.
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Pred. No.
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   PRT;
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SEOUENCE 458 AA; 50771 MW;
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  PRELIMINARY;
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Bacteria; Firmicutes;
Clostridium.
NCBI_TaxID=1492;
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                                                                                                                                             --PKDIILVKGGIA
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                                                                                                                                                                                     --TSYTAILPLLPLS-RVEAQVQRDRVKEELFEVSPKGFWL--
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       Pfam; PF01742; Peptidase_M27; 1.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
SEQUENCE 1255 AA; 143918 MW; 1B557B9D85CD8E4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dong G., Vieille C., Zeikus J.G.; "Cloning, sequencing, and expression of the gene encoding amylopullulanase from Pyrococcus furiosus and biochemical characterization of the recombinant enzyme."; Appl. Environ. Microbiol. 63:3577-3584(1997).

EMBL; AF016588; AAB71229.1; -. SEQUENCE 853 AA; 99035 MW; A25C2C21D2218165 CRC64;
                                                                                                                     Indels
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Archaea; Euryarchaeota; Thermococcales; Thermococcaceae;
NCBI_TaxID=2261;
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                                                                                           5.9%; Score 104.5;
larity 21.9%; Pred. No. 87;
Conservative 67; Mismatches
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Pred. No. 73;
60; Mismatches
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MEDLINE=97438521; PubMed=9293009;
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InterPro; IPR000130;
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640 EPEL---LIPTIL--
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89; Conser
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                                          GYTREDLKTVLYHOMWLLNNTFKEHEKINLLGNGN-----VEVTVVPYAH--PIGPILN
                                                                                                                          281 DFGWSEDFDAHVKK---AHELYKKYLGGGVATPRGGWAAESALNDKTL-EILAENGWQWV
  -DIILVKGGIASDLIEIIGTSYTAILPLLPL--
                                                                                                     ·VSPKGFWLPE--LADPIIPAILKDNGYEYL
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -VQRDRVKEELFEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101;
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                                                                                                                                                                                                                                                                                                                                                                                           229 NILLYGTDIEFIG-YRDIAGRMSVEGLLEVIDELNSELCPS-ELKHSGRELY--
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL162972; CAB86010.1; -.
InterPro; IPR002110; ANK.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
HYPOTHETICAL 79.5 KDA PROTEIN.
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                                                                                                 -SRVEAQVQRDRVKEELFE-
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NCBI_TaxID=3702;
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200 VLLAEDGYHGTLLFLNAIFYRMLGKGFLGIQATHIFGGFDLYLFFFIQLD-IALDLFNMS
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                                                                                                                                                                                                                                                                               --YGTDIEFIGYRDIAGRMSVEGLLE
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                                                                                                            --VLASKPDLFP---GIQVKLPTLPKPSHANKDHKSK
                                                                                                                                                                 -YLLLRELRKAIKLVFEGKVTLKVKDIEAVPVWVAVNTAVMLIGRLPLM
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-VGLAVKGKIREL
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NCBI_TaxID=29292;
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AJ248288; CAB50492.1; -.
InterPro; IPR001696; Na_channel.
PRINTS; PR00170; NACHANNEL.
Hypothetical protein; Complete proteome.
SEQUENCE 394 AA; 43951 MW; 11001889D1AB1165 CRC64;
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                                                                                                                                                                                                                                                                                                                     24 EKAYIPVIETLIKEEP---FGLNITGYTLKFL----PKDIILVKGGIASDLIEIIGTS-Y
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Utterback T., Berry K.,
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                                                                                                                                                                                                                                                                                              Indels
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
NCBI_TaxID=83560;
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                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                              B0C4695613F29219
                                                                                                                                                                STRAIN-KOD1;
Tachibana Y., Fujiwara S., Takagi M., Imanaka
J. Ferment. Bioeng. 83:540-548(1997).
EMBL; D87907; BAA22062.1; -.
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STRAIN=MOPN / NIGG;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., White O., Hickey E.K., Peterson J., Utterbac
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Last annotation
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Fred. No. 63;
67; Mismatches
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
HYPOTHETICAL PROTEIN TC0556
                                               01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2001 (TrEMBLrel. 16, 4-ALPHA-GLUCANOTRANSFERASE.
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                                                                                                   Pyrococcus kodakaraensis
                      PRELIMINARY;
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NCBI_TaxID=69014;
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nes 74; Conser
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01-JAN-1998
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nag
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohluku
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Ogu
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyp
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
EMBL; AP000004; BAA30190.1;
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                                                                                                                                                                                                Length 690;
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                 C., Dods
G., Sal;
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NCBI_TaxID=53953;
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690 AA; 80427 MW; EE12FC17AB8FC3A6 CRC64;
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             Khouri H., Craven B., Bowman & Boy R., Kolonay J., McClarty
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(TrEMBLrel. 14, Last annotation update)
, 37.6 KDA PROTEIN PH1091.
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SEQUENCE 336 AA; 37577 MW; 8256BA1C22B5E817
                                                                                                                                                                                           Score 100.5;
Pred. No. 68;
42; Mismatches
                                                                                  Nucleic Acids Res. 28:1397-1406(2000).
EMBL; AE002323; AAF39395.2; -.
TIGR; TC0556; -.
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Weidman J., Nic.
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                       Gwinn M., Nelson W., DeBoy R.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia
pneumoniae AR39.";
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SEQUENCE 6
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           Linher K.,
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Query Match Best Local Similarity

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MEDLINE=96337999; PubMed=8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                         VFHGNLQYAEIPKSEPKVIEKAYIPVIET ----LIKEEPFGLNITGYTLKFLPKDIILV 59
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN MJ1398,
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206 KERPFVAGTMNP-NYQEKLEGKRLARKIIAGVDVVF-----
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   49;
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EMBL; U67580; AAB99407.1; -.
TIGR; MJ1398; -.
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72;
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--EALYELPEKGEVIARYKDG-KPAAIKINNKI 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                   Amaranthus tricolor (Tampala).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Amaranthaceae; Amaranthus.

NCBI_TaxID=29722;
                                   YL--FADEAMLFS-AHLNSAIKPIKPLPHLIKAQREKRFRYISYLLLRELRKAIKLVFEG
                                                                                    186 KVTLKVKDIEAVPVWVAVNTAVMLIGRLPLMNPKKVASWIEDKNILLYGTDIEFIGYRDI
                                                                   -MLTFQ-
                                                                                                                                                -- LRTSSWADKSLRIWREDEGNA
                                                                                                                                                                       --RELSKNLNKPVSTLTW---HLRILEK----A
                                                                                                                       -LLNDTRREIYNY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEELFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSPK-----GFWLPELADPIIPAILKDNGYEYLFADEAML--FSAHLNSAIKPIKPLPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 DIA---GRMS-VEGLLEVIDELNSELCPSELKHSG--RELYLRTSSWADKSLRIWRE-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| ||::||: |::::||
385 PVADTFGRVNKVEPV--SLEELGRPTVDVVVNCSGVFRDLFINQMNLLDRAVKMLTELDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNDKLTSILGFGLNE-----PWIQYLSNTKFYRADREKLRVLFAFLGECLK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KLVFEGKVTLKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Iwamoto K., Fukuda H., Sugiyama M.;
"Elimination of POR Expression correlates with Red Leaf Amaranthus tricolor.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB050121; BAB41188.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5D262E62BE2343CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 AEIPKSE-PKVIEKAYIPVIETLIKEEPFGLNITGYTLKFLPKDIILV
                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MG-CHELATASE SUBUNIT CHLH (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DLIEIIGTSYTAILPLLPLSRVEAQVQRDRV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VWVAVNTAVMLIGRLPLMNPKKV - - - ASWIEDKNILLYGTD - -
                                                                                                                                                                                             300 RLNMLYNMRGELAFLAENSDARGWPLPERRLDAFRAIY 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                       295 NLIKSKKFGNRLIYYPADMDMRDLPLLYLKNETQKSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99; DB 1
Pred. No. 72;
52; Mismatches
                                                                                                                -ETLKKKFLELISALASVK - - VFILSRINLLDEEKV - -
                                                                                                                                          246 AGRMSVEGLLEVIDELNSELCPSELKHSGRELY --
                                                       171 YVGFKPDEDVLANLIYIHIVKKTSNPLPYIL--
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                                                      ---ILDNPGCHL---
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67073 MW;
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| | | | .:::|
118 REVNGNKTIIWIKDPLKLKQSEV
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608 AA;
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les 79; Conser
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01-JUN-2001
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | || : | : | : | : | DFPKIPKSTEVKEFISQAVLKNNFLKHL--EECQVKEIVLFMSQKSFKRGEYIIKEGDMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --GIASDLIEIIGTSYTAILPLLPLSRVEAQVQR----DRVKEELFEVSPK-GFWLPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 NVFQAVMQKTGIMRREEHYNFLHSVPVFKNLPNDTLLKIVEVIEEE----FYEDGEFIVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AILKDNGYEYLFADEAMLFSAHLNSAIKPIKPLPHLIKAQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LIGRLPLMNPKKVASWIEDKNILLYGTDIEFI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TLKVKDIEAVPVW----
                                                                                                                                                                                             Hydra oligactis (Hydra).
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
Hydridae; Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF0000; CNMr; _ SMART; SM00100; CNMr; _ SMART; SM00220; S_TKc; 1.

R SMART; SM00133; S_TK_X; 1.

R PROSITE; PS00088; CNMP_BINDING_1; 1.

R PROSITE; PS00092; NG_MTASE; UNKNOW_1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; TONB_DEPENDENT_REC_1; UNKNOWN_1.

PROSITE; PS00430; TONB_D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LQYAEIPKSEPKVIEKAYIPVIETLIKEEPFGLNITGYTLKF--LPKDIILVKG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GYRDIAGRMSVEGLLEVIDELNSELCPSELKHSGRELYLRTSSWADKSLR 290
                                                                                                                                                                                                                                                                                                                                                                     litted (OCT-1997) to the EMBL/GenBank/DDBJ databases. SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES. FAF031931; AAC23588.1; -. P05132; 1ATP.
                                                                                                                                            update)
                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 99; DB 5; Le
Pred. No. 96;
); Mismatches 133;
                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
CYCLIC GMP-DEPENDENT PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002290; Ser_thr_kin_actsite.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00027; cNMP_binding; 2.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000595; cNMP_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000719; Euk_pkinase.
IPR002052; N6_Mtase.
IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFRYISYLLLRELRKAIKLVFEGKV---
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nilarity 21.7%;
Conservative 60
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                                              PRELIMINARY;
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IPR002290;
IPR000531;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VAVNTAVM--
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=6088;
                                        017474
017474;
01-JAN-1998
01-JAN-1998
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 15
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RESULT
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14;

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DD 309 EGERGDSFYILKQGLVKVLQMIEGKDEPVEIRHLSQGEYFGEKALLGEDVR 359

Search completed: April 4, 2002, 14:44:28 Job time: 252 sec

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4.5
Compugen Ltd.
 version - 2000
 GenCore
Copyright (c) 1993
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model Ν using protein search, OM protein

Search time 25.55 Seconds
(without alignments)
1003.106 Million cell updates/sec 2002, 14:41:21; 4 April Run on:

US-09-407-806A-4 score: Perfect Title:

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522463 seqs, Searched:

74073290 residues 0 Word size 522463

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

summaries Post-processing: Listing first 45

Database

A\_Geneseq\_1101:\*

| SIDS2/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
| SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution. greater Pred. No and is score

## SUMMARIES

		Description	Thermostable alaba	L. Jactis MG1316 A	Chlamydia nneumoni	Human colon cancer	Amino acid secuence	Arabidonsis thalia	Arabidonsis thalia	Arabidonsis thalia	Arabidopsis thalia	Human secreted pro	Human 5' EST secre
		QI	8 AAW34643		_			-		-	1 AAG40492		0 AAY12375
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<b>*</b> P	Query	Match Le	5.5	2.3	2.3	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0
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## ALIGNMENTS

Alpha-galactosidase; alpha-glycosidase; thermostable enzyme; food processing; alpha glycoside hydrolysis; raffinose; stachyose; verbascose; bean; flatulence; AEDII12RA-alpha-gal-18GC. Thermostable alpha-galactosidase AEDII12RA-alpha-gal-18GC. Thermococcus alcaliphilus strain AEDII12RA Key Location/Qualifiers Misc-difference 329 AAW34643 standard; Protein; 364 AA (first entry) 27-MAR-1998 AAW34643; AAW34643 

/note= "encoded by CTT" (RECO-) RECOMBINANT BIOCATALYSIS INC. 97WO-US01452. 96US-0613220. W09732974-A1 12-SEP-1997. 05-FEB-1997; 08-MAR-1996;

Rudolph MJ; WPI; 1997-470541/43. N-PSDB; AAT93753. Reid J, Murphy D,

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Local Similarity
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactic acid; food industry; food-grade inducer; cheese production; rnhB; gadR; gadC; orfX; rggL.
                                                                                                          This protein comprises AEDII12RA-alpha-gal-18GC, a claimed
thermostable alpha-galactosidase of Thermococcus alcaliphilus
AEDII12RA, a bacterium that shows optimum growth at 85 deg C and
pH 9.5. Also claimed are: (1) an isolated polynucleotide (see
ATT93753) encoding the alpha-galactosidase; (2) a vector containing
the polynucleotide or homologous or complementary sequences; (2)
host cells containing the vector; (3) a process for producing the
alpha-galactosidase in transformed or transfected host cells; an
enzyme showing at least 70% identity to alpha-galactosidase and
comprising at least 30 amino acid residues of its sequence; and (4)
a method for hydrolysing alpha-galactoside bonds using the enzyme.
The enzyme can be used to hydrolyse raffinose to sucrose and glucose in sugar beet processing (raffinose inhibits crystallisation of sucrose), and as a digestive aid to hydrolyse raffinose, stachyose and verbascose in beans and other gassy foods.
                                                                                                                                                                                                                                                                                                       glucose
of
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                                                                                                                                                                                   taining
                                                                                                                                                                                                                                                                      and (4)
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                   Thermococcus
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                                 to hydrolyse
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 18;
Pred. No. 1.7e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from lactic peptides in food
                   from
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                encoding alpha-glycosidase - used in food processing tides, e.g. raffinose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inducible promoter - derived from the production of polypeptides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              466 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanders JW,
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0
                                                                                  Claim 1; Fig 1; 32pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5%;
100.0%;
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96EP-0202444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
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Les 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                        364 AA;
                                               alpha-glycosides,
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                 Nucleic acid
alcaliphilus
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05-SEP-1996;
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from the NS3 locus of the lactic acid bacterium Lactococcus lactis. This fragment also contains the C-terminus of rnhB, full length gadR protein (also known as rggL), gadC protein (also known as orfX) and the C-terminus of an unknown reading frame which reads in the reverse orientation. This fragment is also found to act as a salt-inducible promoter (SIP). Using this SIP, salt can be used as a food-grade inducer in food fermentation processes, e.g. in the production of cheese, dressings, water-containing spreads, sausages, or sour dough.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; pneumonia; bronchitis; heart disease; sarcoidosis; purulent otitis media; erythema nodosum; pharyngitis;
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C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions, especially where the vector directs the expression of a neutralising
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                      Length 466;
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                                                                                                                                                                                                                                                                                                                                                      Score 8; DB 1; Pred. No. 19; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                                                                                                                                                            0;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0107078
97FR-0014673
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8; Conser
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50 AA;
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                                                                                                   06-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                             Gallus sp.
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                                                                           AAB30440;
                                                 AAB30440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>;</del>
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                                                                                                                                                                                                                         colon cancer; colon cancer antigen; diagnosis; detection;
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  Indels
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                                                                                                                                                                                               Human colon cancer antigen protein SEQ ID NO:8418
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Pred. No. 22;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEO ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                   CA;
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acids encoding 4277 human colon coor preventing, diagnosing and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
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99US-0163280.
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                                                                                                                   standard; Protein;
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N-PSDB; AAH37059.
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03-NOV-1999;
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AAB30440-85 represent peptides derived from galectin family members. Galectin-3 has been associated with assorted processes such as cell growth, tumour transformation, and metastasis. It is composed of two domains: a carbohydrate-binding region on the carboxy terminal which binds saccarides with terminal galactose residues, and an amino terminal domain consisting of tandem repeats of nine amino acids. The expression of galectin-3 is induced in cirrhotic liver and hepatocellular carcinoma. Galectin-3 is used in diagnostic, prognostic and therapeutics for the treatment and prevention of hepatocellular carcinoma. It is useful for determining whether an individual is suffering from hepatocellular carcinoma or is likely to suffer from hepatocellular carcinoma or any neoplasm of liver origin or cirrhosis of
                                                                                                                                                                                                               cirrhotic liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 24;
0; Mismatches
                                                                                                                                                         Amino acid sequence of a fragment of
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standard; peptide;
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pathway;
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PR 24-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140895.
PR 24-JUN-1999; 99US-0140895.
PR 29-JUN-1999; 99US-0141842.
PR 30-JUN-1999; 99US-0141842.
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PR 01-JUL-1999; 99US-0142370.
PR 13-JUL-1999; 99US-0142371.
PR 13-JUL-1999; 99US-0144083.
PR 13-JUL-1999; 99US-0144332.
PR 13-JUL-1999; 99US-0144332.
PR 15-JUL-1999; 99US-0144332.
PR 15-JUL-1999; 99US-0144332.
PR 15-JUL-1999; 99US-0144332.
PR 15-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 21-JUL-1999; 99US-0144332.
PR 21-JUL-1999; 99US-0144332.
PR 22-JUL-1999; 99US-0144332.
PR 22-JUL-1999; 99US-0144333.
PR 22-JUL-1999; 99US-014508.
PR 22-JUL-1999; 99US-014508.
PR 22-JUL-1999; 99US-014508.
PR 22-JUL-1999; 99US-014538.
PR 22-JUL-1999; 99US-014338.
PR 22-JUL-1999; 99US-014935.
PR 22-JUL-1999; 99U
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pathway;
promoter;
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99US-0161359.
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20-SEP-1999;
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PR 15-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144085.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144331.
PR 20-JUL-1999; 99US-0144331.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 20-JUL-1999; 99US-0144332.
PR 21-JUL-1999; 99US-0144332.
PR 22-JUL-1999; 99US-014508.
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PR 22-JUL-1999; 99US-014508.
PR 22-JUL-1999; 99US-014508.
PR 23-JUL-1999; 99US-014508.
PR 23-JUL-1999; 99US-014518.
PR 23-JUL-1999; 99US-014518.
PR 23-JUL-1999; 99US-014518.
PR 23-JUL-1999; 99US-014519.
PR 23-JUL-1999; 99US-014919.
PR 23-JUL-1999; 99US-015108.
PR 23-JUL-1999; 99US-0152108.
PR 23-JUL-1999; 99US-0

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Pred. No. 49;
0; Mismatches
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99US-0161405.
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99US-0144333.
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99US-0144352.
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99US-0144684.
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99US-0151339.
99US-01514739.
99US-0151889.
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21-SEP-1999;

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forensic; gene therapy; chromosome mapping; signal peptide; unagnosis; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
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                                                                                                                                                                                                                                                                                                                                                                     Length 108;
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red. No. 49;
Mismatches
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Pred.
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99us-0159295.

99us-0159329.

99us-0159331.

99us-0159637.

99us-0159638.

99us-0159638.

99us-0160741.

99us-0160741.

99us-0160770.

99us-0160814.

99us-0160989.

99us-0161404.

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N-PSDB; AAX51955.
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14-OCT-1999;
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regulating,

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human secreted proteins, and encode the proteins given in AAY12987 to AAY13219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone capulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products activity, the used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                           for
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Gaps ô Length 113; Indels ; 0 DB 20; . 51; Score 7; DB 2; Pred. No. 51; 0; Mismatches 2.0%; SU 100.0%; PJ 0; Conservative Local Similarity 76 TAILPLL 82 7; Query Match , Matches ŏ

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AAY12375 RESULT

AAY12375 standard; Protein; 116 AA. (first entry) 17-JUN-1999

haemostatic; egulation; feration; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell prolif differentiation; haematopoiesis regulation; tissue growth rereproductive hormone regulation; chemotactic; chemokinetic; thrombolytic; anti-inflammatory; tumour inhibition. expressed sequence tag; secreted protein; EST;

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secreted protein SEQ ID NO:406.

Human 5' EST

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WO9906548-A2 

11-FEB-1999

98WO-IB01222 31-JUL-1998;

97US-0905135 01-AUG-1997; XX PF XX XX XX XX

(GEST ) GENSET

Lacroix B; Dumas Milne Edwards J, Ą Duclert

1999-153778/13. N-PSDB; AAX41208

from obtained New nucleic acids encoding human secreted proteins - obtaine cDNA libraries prepared from e.g. liver, ovary, brain, prost kidney, lung, umbilical cord, placenta and colon tissue

Claim 27; Page 727-728; 824pp; English

called pancreatic cancer antigens, given in AAB54008

proteins,

human secreted proteins, and encode the proteins given in AAX12261 to
AAV12514, respectively. The proteins given represent the signal peptide
and an N-terminal fragment of a secreted brown in The nucleic acid
sequences can be used for producing secreted human gene products. They
can also be used to develop products for diagnosis and therapy. The
proteins obtained may have cytokine activity, cell
proliferation/differentiation activity, haematopoiesis regulating
activity, tissue growth regulating activity, reproductive hormone
regulating activity, chemotactic/ chemokinetic activity, haemostatic and
thrombolytic activity, receptor/ ligand activity, anti-inflammatory
activity, tumour inhibition activity or other activities. The products
can be used in forensic, gene therapy and chromosome mapping procedures.
The sequences can also be used for obtaining corresponding promoter
sequences. The nucleic acids encoding the signal peptide can be used for
directing extracellular secretion of a polypeptide into a cell. tags (ESTs) for n in AAY12261 to Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic; neural; immune system; muscular; reproductive; gastrointestinal; pulmonary; cardiovascular; renal; proliferative. New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition AAC98773 to AAC99231 encode the human pancreatic cancer associated Human pancreatic cancer antigen protein sequence SEQ ID NO:879. .; 0 Length 116; Indels sedneuce 0; DB 20; . 52; expressed Score 7; DB 2 Pred. No. 52; 0; Mismatches 1379pp; English. AAB54427 standard; Protein; 138 AA. AAX41094 to AAX41347 represent 5' · () 2.0%; 100.0%; (HUMA-) HUMAN GENOME SCI INC 2000WO-US05989. 99US-0124270. (first entry) Conservative Ruben SM; Claim 11; Page 1339; 2000-579444/54. Similarity 7; Conser 116 AA; AAC99192. 76 TAILPLL 82 WO200055320-A1. Homo sapiens, 08-MAR-2000; 12-MAR-1999; 21-SEP-2000. 09-MAR-2001 AAB54427; Sequence Rosen CA, Local N-PSDB; Matches WPI; AAB54427 888888888888888888888888888 pp XX Κ PF XX

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AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be used in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used to detect, treat or prevent pancreatic disorders, especially cancer. Agonists and antagonists to the antigens can be used to design nucleic acid hybridisation probes, that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic
                                                                                                                                                                                                                                                                                      system, muscular,
r, renal or
67 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
                                                                                                                                                                                                                             and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
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n pathway; metabolic pathway; expression control; promoter;
can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
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